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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOURCE ORGANISM ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	RESULT 1 AX179789 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	444443333333 5422109875	c 224 4 22 2 2 2 1 1 1 7 2 2 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3		Result No.
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JOURNAL Genomics 72 (2), 119-127 (2001)

MEDLINE 21295030

REFERENCE 2 (bases 1 to 694)
AUTHORS Liang, Y. and Tedder, T.F.

TITLE Direct Submission
Direct Submitted (24-FEB-2000) Immunology, Duke Medical Center, Research
Source /organism="Homo sapiens"
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CDS /55.657

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VLFLGILITLMTFSIIELFISLPFSIIGCHSEDCDCEQCC"

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Submitted (14-NOV-2000) Division of Immunology and Cell Biology,
John Curtin School of Medical Research, Mills Road, Canberra, ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 697)

Hulett.M.D., Pagler,E., Hornby,J.R., Hogarth,P.M., Eyre,H.J., Baker,E., Crawford,J., Sutherland,G.R., Ohmes,S.J. and Parish,C.R. Isolation, tissue distribution, and chromosomal localization of a novel testis-specific human four-transmembrane gene related to CD: and Popping and PropositionRI-beta
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RKMKILGTIQILFGIMTFSFGVIFLFTLLKPVPRFPFIFLSGVPFWGSYLFINSGAFL
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VLLLGILITLMTFSIELFISLFFSILGCHSEDCDCEQCC"

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/product="testis-expressed transmembrane-4
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Homo sapiens
AB013103
                                                                                                                                                             Submitted (20-APR-1998) Kenichi Ishibashi, Tokyo Medical and Dental University, 2nd Internal Medicine; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:kishibashi.med2@med.tmd.ac.jp, Tel:81-3-5803-5223, Fax:81-3-5803-0132)
                                                                                                                                                                                                                                                                                                                                                                     Ishibashi, K., Suzuki, M., Sasaki, S. and Imai, M. Identification of a new multigene four-transmembrane family related to CD20, HTm4 and beta subunit of the high-affinity
                                                                                                                                                                                                                        Direct Submission
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Cloning of three CD20
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21142397
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MS4A5; CD20-like
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/codon_start=1
/product="MS4A5"
                          /gene="MS4A5"
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/db_xref="GI:11559214"
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RKMKILGTIQILEGIMTESFGVIFLFTLLKPYPRFPFIFLSGYPFWGSVLFINSGAFL
IAVKRWTETLILLSRIMNFLSALGAIILLTFGFILDQNYICGYSHQNSQCKAVT
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Walke, D.W. and Turner, C.A.
Human membrane proteins and polynucleotides encoding having homology to cd20 proteins and ige receptors Patent: WO 0146417-A 1 28-JUN-2001;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
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                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhin; Hominidae;
1 (bases 1 to 417)
Walke,D.W. and Turner,C.A.
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1 (bases 1 to 450)

Walke,D.W. and Turner,C.A.

Human membrane proteins and polynucleotides encoding the same having homology to cd20 proteins and ige receptors

Patent: WO 0146417-A 7 28-JUN-2001;
                                                                                        Human membrane proteins and polynucleotides encoding having homology to cd20 proteins and ige receptors Patent: WO 0146417-A 5 28-JUN-2001;
                                                                                                                                                                                                                         AX179785 417 bp DNA
Sequence 5 from Patent WOO146417.
AX179785.1 GI:15132146
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             /organism="Homo sapiens"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 246)
Walke,D.W. and Turner,C.A.
Human membrane proteins and polynucleotides encoding having homology to cd20 proteins and ige receptors Patent: WO 0146417-A 3 28-JUN-2001;
Lexicon Genetics Incorporated (US)
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Sequence 3 from Patent WO0146417
AX179783
AX179783.1 GI:15132145
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boguslavkiy, L., Boukhgalter, B., Brown, A., Bulnett, C., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Heaford, A., Horton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 18, 2000 this sequence version replaced gi:7382629. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Boouslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Colangelo, M., Collins, S.,
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                                                                                                                                                             NOTE: This record contains 163 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                      However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: 19008
Center clone name: 196_E_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submission
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J., Barna,N., Bastien,V., Beda,F.,
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20436: gap of 100 bp
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37892: contig
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37208: gap of 100 bp
37892: contig of 684 bp in length
37992: gap of 100 bp
37892: contig of 680 bp in length
3872: gap of 100 bp
38772: gap of 100 bp in length
38775: contig of 703 bp in length
39475: contig of 703 bp in length
40290: contig of 715 bp in length
40390: gap of 100 bp
40390: gap of 100 bp
40390: gap of 100 bp
41891: contig of 688 bp in length
41891: gap of 100 bp
41891: contig of 688 bp in length
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42679: contig of 688 bp
2779: gap of 100 bp
43500: contig of 721 bp in
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100 bp
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5783: gap of 100 bp

47481: contig of 698 bp 1.

7581: gap of 100 bp

48290: contig of 709 bp 11

3390: gap of 100 bp

49077: contig of 687 bp 11
                                                                                                                                                                                                                                                                                                                    44295: contig of 695 bp 1
4395: gap of 100 bp
4396: contig of 693 bp 1
5188: gap of 100 bp
45880: contig of 692 bp 1
5980: gap of 100 bp
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Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Tralamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-AFR-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA on Aug 18, 2000 this sequence version replaced g1:7382629. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,Y., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
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Birren, B., Linton, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 15, clone RP11-196E16
NOTE: This record contains 163 individual sequencing reads that have not been assembled into sequencing reads that used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows in the partial sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
------ project Information
Center project name: L9008
Center clone name: 196_E_16
                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
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* However, it should
* will be sequenced
* the record is upda
* be preserved.
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26865: ga
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1564: gap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Allen,N., Anderson,M.,
Bairen,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassillev,H., Vo,A., Wheeler,J., Wu,X.,
Pollara,V., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGGGGTAAGTAAGA 112383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 27, 2000 this sequence version replaced gi:6446828. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum
Homo sapiens, clone RP11-24D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC015840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC015840.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 147788)
Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 136347 bases at least Q40
Consensus quality: 143600 bases at least Q30
Consensus quality: 146212 bases at least Q20
Insert size: 203000; agarose-fp
Insert size: 147388; sum-of-contigs
Quality coverage: 5.2 in Q20 bases; agarose-fp
                                                                                                                                                                                                       Center project name: 14434
Center clone name: 24_D_1
------ Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147788 bp DNA HTG 27-APR-2000 ns clone RP11-24D1, WORKING DRAFT SEQUENCE, 5 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:7657730
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                                                                                                                                                                                                                                                                                                                                                                                                          for Genome Research
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                          VERSION
KEYWORDS
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AP003127/c
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Matches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                      1 tcatctcctttcaaattatcaccgacaccatcatggattcaagcaccgcacacagtccgg 60
                                                                                                                                                                                                                                                                    TAGGGGTAAGTAAGA 128209
                                                                                                                                                                                                                                                                                                                                                                                                           TCATCTCCTTTCAAATTATCACCGACACCATCATGGATTCAAGCACCGCACACAGTCCGG 128074
                                                                                                                                                                                                                             tagggactatccaga 195
                                                                  AP003127 161039 bp DNA
Homo sapiens chromosome 11 clone
SEQUENCE, 15 unordered pieces.
AP003127.1 GI:12597183
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-710G6
                                                       AP003127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 7.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16188 16287: gap of 100 bp
16288 25089: contig of 8802 bp in length
25090 25189: gap of 100 bp
25190 25199: gap of 38734 bp in length
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6695 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
64024. .147788
/note="assembly_fragment"
29482 c 28861 g 43569 t
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25190. .63923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_end:SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-24D1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-11 Human
1, .6594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.4%;
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34: gap of 100 bp
16187: contig of 993 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .25089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 100 bp
contig of 83765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 185.4; DB 2
Pred. No. 3.8e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                      HTG
RP11-710G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Male
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 147788;
                                                                                      map 11q,
                                                                                      30-JAN-2001
.q, WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                          128134
                                                                                        DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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JOURNAL REFERENCE

TITLE

AUTHORS

TITLE JOURNAL

COMMENT

Web site:

REFERENCE AUTHORS

ORGANISM

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* NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 15 configs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Only in DataBase (2001) In press 2 (bases 1 to 161039)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-JAN-2001) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. a Homo sapiens 161,039 genomic DNA of 11q
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15 contigs. The true order of the pieces i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: HumDraft11
Center clone name: RP11-71066
Center clone name: RP11-71066
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0,990329
Consensus quality: 157456 bases at least Q40
Consensus quality: 159450 bases at least Q30
Consensus quality: 159457 bases at least Q20
Insert size: 15639; sum-of-contigs
Quality coverage: 8.61x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 161039)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: RIKEN Genomic Sciences Center(GSC)
                  42323 42422: contig of 42322 bp in length
42323 42422: gap of 100 bp
42423 63418: contig of 20996 bp in length
63419 63518: gap of 100 bp
63519 77969: contig of 14451 bp in length
77970 78069: gap of 100 bp
78070 93182: contig of 15113 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as it is available and the accession number will be
      93282:
                                                                                                                                                                                                                                                                                                             104093 contig of 115702 contig of 125183 contig of 132558 contig of 137219 contig of 143276 contig of 148922 contig of 154159 contig of 159134 contig of 159234 contig of 159234 contig of 159234 contig of 159234 contig of
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gap of
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7275 bp
4567 bp
5957 bp
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and Sakaki, Y.
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137320. .143276
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                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-JAN-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
On Nov 14, 2000 this sequence version replaced gi:8117704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 166,804 genomic DNA of 11q12
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AP001034.4 GI:11176992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Only in DataBase (2000) In press 2 (bases 1 to 166804)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hattori@gsc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://hgp.gsc.riken.go.jp/
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Center code: RIKEN
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149455 154522 contig of 5068 bp in length
154623 155919 contig of 1297 bp in length
156020 159504 contig of 3485 bp in length
159605 159679 contig of 75 bp in length
159780 162418 contig of 2639 bp in length
162519 165383 contig of 2865 bp in length
162519 165383 contig of 1321 bp in length
165484 166804 contig of 1321 bp in length
165484 166804 contig of 1321 bp in length
165486 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64279 64378; gap of 100 bp 64279 77579; contig of 13201 bp in length 77580 77679; gap of 100 bp 100 pp 100 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159680 159779: gap of 100 l
159780 162418: contig of 2639
162419 162518: gap of 100 l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155920 156019:
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22399 22498: gap of 100 bp
22499 45238: contig of 22740 bp in length
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                                         /note="assembly_fragment"
93819. .108057
                                                                                       /note="assembly_fragment" 77680. .93718
                                                                                                                                       64379.
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                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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                   'note="assembly_fragment"
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144653: contig of 4128
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9454: gap of
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155919: contig
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                                                                                                                                                                                     .64278
                                                                                                                                                                                                                                 .45238
                                                                                                                                       .77579
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contig of 75 bp in length
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6846 bp in length
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGGGGTAAGTAAGA 11593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCACGACCTTTTCAACTCAAAGCCCCCTTGCAAAAATTATTTTGCTAGAAAATGAAAATCT 11608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTTTCTGGTATTTCCTCCAGAAATCACTGCTTCAGAATATGAGTCCACAGAACTTTCAG 11668
2 (bases 1 to 166820)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S. Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.
                                                                                                                                  Homo sapiens chromosome 11, clone RP11-729B4 Unpublished
                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome 11 clone RP11-729B4 SEQUENCE, 2 ordered pieces
                                                                                                                                                                         1 (bases 1 to 166820)
Birren,B., Linton,L.,
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                      Homo sapiens
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/note="assembly_fragment"
a 31523 c 32296 g 50478
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159780. .162418
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144754. .149354
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117107. .126302
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154623. .155919
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Center project Information

Center project name: 112709

Center clone name: 729_B.4

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 166378 bases at least Q40

Consensus quality: 16639 bases at least Q20

Insert size: 116700; agarose-fp

Quality coverage: 12.2 in Q20 bases; sum-of-contigs

Quality coverage: 12.9 in Q20 bases; sum-of-contigs
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1095: contig of 1095 bp in length
1096 1195: gap of 100 bp
1196 16820: contig of 165625 bp in length.
Location/Qualifiers
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                                                        46436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    provided by the submittor. This sequence will be replaced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
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                                             vector_side:right"
31826 c 32895 q
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1196. .166820
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                                                                                                                                                                                                                                                                                                                                                 1. .1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP11-729B4"
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                                             100 others
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27.48;

Score 185.4;

DB <u>ب</u>

Length 166820;

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REFERENCE
AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 tgtttctggtatttcctccagaaatcactgcttcagaatatgagtccacagaactttcag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 tcatctcctttcaaattatcaccgacaccatcatggattcaagcaccgcacacagtccgg
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                                                                             15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-JAN-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 161039)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 161,039 genomic DNA of 11q
published Only in DataBase (2001) In press
2 (bases 1 to 161039)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG 30-JAN-2001
Homo sapiens chromosome 11 clone RP11-710G6 map 11g, WORKING DRAFT SEQUENCE, 15 unordered pieces.
APP03127
                                                                                                                                              NOTE: This is a 'working draft' 15 contigs. The true order of the
                                           preserved
                                                              as soon as it is available and the accession number will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                             Center project name: HumDraftl1 Center clone name: RP11-710G6 ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
------ Project Information
                                                                                                                                                                                                                                              Assembly program: Phrap; version 0.990329
Consensus quality: 157456 bases at least Q40
Consensus quality: 158960 bases at least Q30
Consensus quality: 159457 bases at least Q20
                                                                                                                                                                                                                                                                                                                                Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of
                                                                                                                                                                                                          Quality coverage: 8.61x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: RIKEN Genomic Sciences Center(GSC)
                                                                                                                                                                                                                               Insert size: 159639; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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    42423
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42322 contig of 63418 contig of
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42322 bp
20996 bp
                                                                                                                                                                 sequence. It currently consists of
o in length
o in length
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NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149023 154159: contig of 51
154160 155259: gap of 10
154260 157686: contig of 34
157687 157786: gap of 17
157787 159234: contig of 17
159235 159334: gap of 17
159335 161039: contig of 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137220 137319; gap of 100 bp
137320 143276; contig of 5957 bp in
143277 143376; gap of 100 bp
143377 148922; contig of 5546 bp in
148923 149022; gap of 100 bp
149023 154159; contig of 5137 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93183 93282; gap of 100 bp

93283 104093; contig of 10811 bp in length

104094 104193; gap of 100 bp

104194 115702; contig of 1509 bp in length

115703 115802; gap of 100 bp

115803 125183; contig of 9381 bp in length

115803 125183; contig of 9381 bp in length
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115803
125284
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125284 132558: contig of 7275 bp
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63519 77969: contig of 14451 bp in length
77970 78069: gap of 100 bp
78070 93182: contig of 15113 bp in length
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42423 63418: contig of 20996 bp in length
                                                            /note="assembly_fragment"
115803. .125183
                                                                                                  /note="assembly_fragment"
104194. 115702
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93283. .104093
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                     /note="assembly_fragment"
125284. .132558
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78070. .93182
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="assembly_fragment"
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63519. .77969
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100 bp
148 bp ;
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3427 bp
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10811
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115113 bp
1108113 bp
110811 bp
11509 bp
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7275 bp
4561 bp
5546 bp
5546 bp
5137 bp
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3427 bp
1448 bp
1705 bp
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ALIGNMENTS

RESULT AAS04283 22-DEC-1999; 12-DEC-2000; 2000WO-US33742 Human; membrane protein; membrane receptor; IgE receptor; CD20; physiological disorder; ds. 28-JUN-2001. WO200146417-A2 Homo sapiens. DNA sequence encoding novel human membrane 26-SEP-2001 AAS04283; AAS04283 standard; DNA; 676 _ (first entry) 99us-0171567 ВP

protein

Polynucleotide encoding novel human membrane protein, useful for identifying agonist, antagonist or modifiers or for producing antibodies useful in therapeutic, diagnostic and pharmacogenomic applications WPI; 2001-408646/43.

Walke DW,

Turner CA;

(LEXI-) LEXICON GENETICS INC

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                                                                                                                                                                                                                                                   The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For CENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate CENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be presence of similar nucleic acid sequences in samples, and hence to the GENSET polypeptides may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antipodies and in assays to identify modulators (agonists and cantipodies) of GENSET polypeptide expression and activity. The present sequence is a GENSET nucleic acid of the invention.
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Best Local S
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                                                                                                                                                                                                                               Sequence
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                                                                                                                                                             Score 668; DB 22;
Pred. No. 5.7e-172;
0; Mismatches 5;
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WPI; 2001-408646/43
P-PSDB; AAU01210.
                        Walke
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                       DW,
                                                                                                                                                                            membrane protein logical disorder;
                                      LEXICON
                       Turner CA
                                                                    2000WO-US33742
                                                                                                                                                                                                                   (first entry)
                                                     99US-0171567
                                      GENETICS
                                                                                                                              Location/Qualifiers
1..603
/*tag= a
                                                                                                                                                                                    protein; membrane receptor;
                                                                                                               /*tag= a
/product= "Human membrane protein #1"
/transl_except= (pos:595..600,aa:Cys)
                                                                                                                                                                                                                                                   cDNA;
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                                                                                                                                                                                   IgE
                                                                                                                                                                                    receptor;
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The present sequence encodes for novel human membrane protein #1. Human membrane protein #1 is 1 of 4 human membrane proteins (AAU01210-AAU01213) given in the present invention. These membrane proteins share structural similarity with membrane receptors such as the IgE receptor and mammalian CD20. The novel human membrane proteins are useful for identifying agonists, antagonists and modulators of the membrane proteins, and for producing antibodies specific to the drug screening, pharmacogenomic applications, clinical trial monitoring and the treatment of physiological disorders and diseases. The polynucleotides encoding the membrane proteins can be used to generate polynucleotides encoding the membrane proteins can be used to generate polynucleotides on probes to identify mutations associated with a particular disease.
                                                                                                                                                                                                                                                                                                                                        Polynucleotide encoding novel human membrane identifying agonist, antagonist or modifiers antibodies useful in therapeutic, diagnostic applications
     Sequence
                                                                                                                                                                                                                                                                                                         Claim 1;
     603
                                                                                                                                                                                                                                                                                                         Page 29;
     ₿₽;
     162
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     other;
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Query Match Best Local S Matches 603

Similarity

89.2%; ilarity 100.0%; Conservative (

0;

Mismatches

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Score 603; DB 22; 1 Pred. No. 2.4e-154;

Length Indels

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γQ Qy Вþ В γ 맑 В δÃ DЬ Ş 밁 Qy В Ş Qy 밁 Ş В Qγ 밁 Qy 밁 633 541 481 513 421 453 361 393 301 333 241 273 181 213 121 153 61 93 ü gtcctgttcttgggaattttgattacattgatgactttcagcattattgaattattcatt atggattcaagcaccgcacacagtccggtgtttctggtatttcctccagaaatcactgct atggattcaagcaccgcacacagtccggtgtttctggtatttcctccagaaatcactgct tga gtcctgttcttgggaattttgattacattgatgactttcagcattattgaattattcatt ctagatcaaaactacatttgtggttattctcaccaaaatagtcagtgtaaggctgttact ctagatcaaaactacatttgtggttattctcaccaaaatagtcagtgtaaggctgttact aatcttcttagtgccctgagagcaatagctggaatcattctcctcacattttggtttcatc ttcctaattgcagtgaaaagaaaaccacagaaactctgataatattgagccgaataatg tttatatttctttcaggatatccattctggggctctgttttgttcattaattctggagcc tttatatttctttcaggatatccattctggggctctgtttttgttcattaattctggagcc tcagaatatgagtccacagaactttcagccacgaccttttcaactcaaagccccttgcaa 152 aatcttcttagtgccctgagagcaatagctggaatcattctcctcacatttggtttcatc ttcctaattgcagtgaaaagaaaaccacagaaactctgataatattgagccgaataatg tcagaatatgagtccacagaactttcagccacgaccttttcaactcaaagccccttgcaa 635 512 452 120 60 480 420 360 392 300 240 180 212 332 272

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                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                     The present sequence encodes for novel human membrane protein #4. Human membrane proteins (AAU01210-AAU01213) given in the present invention. These membrane proteins (PAU01213) given in the present invention. These membrane proteins share structural similarity with membrane receptors such as the IgE receptor and mammalian CD20. The novel human membrane proteins are useful for identifying agonists, antagonists and modulators of the membrane proteins, and for producing antibodies specific to the membrane proteins. The membrane proteins can be used for diagnosis, drug screening, pharmacogenomic applications, clinical trial monitoring and the treatment of physiological disorders and diseases. The polynucleotides encoding the membrane proteins can be used to generate PCR primers or probes to identify mutations associated with a particular plant of the process of the membrane proteins can be used to generate polynucleotides and the treatment of physiological disorders and diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide encoding novel human membrane protein, useful for identifying agonist, antagonist or modifiers or for producing antibodies useful in therapeutic, diagnostic and pharmacogenomic
                                                                                                                                                                                                                               Sequence 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-1999;
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                                                                                                                                                        Conservative
                                                                                                                                                                                                                               BP; 120 A; 94 C;
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disorder; ss.
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97.0%;
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                                                                                                                                                                     Score 347.4; DB 1
Pred. No. 5.9e-85;
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                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                               159 T; 0 other;
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P-PSDB; AAU01212.
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physiological disorder; ss.
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                                                                                                                                        applications
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                                                                                                                                                                                                                                         (LEXI-) LEXICON GENETICS
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/product= "Human membrane protein
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The present sequence encodes for novel human membrane protein #3. Human membrane protein #3 is 1 of 4 human membrane proteins (AAU01210-AAU01213) given in the present invention. These membrane proteins share structural similarity with membrane receptors such as the IgE receptor and mammalian CD20. The novel human membrane proteins are useful for identifying agonists, antagonists and modulators of the membrane proteins, and for producing antibodies specific to the membrane proteins. The membrane proteins can be used for diagnosis, drug screening, pharmacogenomic applications, clinical trial monitoring and the treatment of physiological disorders and diseases. The

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Best Local Similarity
Matches 343; Conserv
  mRNAs encoding secreted
           The present sequence is
                               Claim 1; SEQ
                                                 New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond diagnostic, forensic, gene therapy and chromosome
                                                                                                                        Dumas
                                                                                                                                                                                21-FEB-2000; 2000EP-0200610
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                                                                                                                                                                                                                                                                 gene
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                                                                                          2000-500381/45
DB; AAG03074.
                                                                                                                                                                                                                                                                therapy;
                                                                                                                                                                                                                                                                                                                                                                                                          accttttcttttggagttatcttccttttcaccttgttaaaaccatatccaaggtttccc
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                                                                                                                       Milne Edwards
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                                                                                                                                                                                                                                                                         EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP;
                             ID 3078; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                 chromosome
                                                                                                                                                               9908-0122487
                                                                                                                                                                                                                                                                                               protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115
                                                                                                                                                                                                                                                                                                                                                           cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
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one of a large number of 5' \mathtt{ESTS} derived from proteins. An ORF has been identified within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
                                                                                                                       Duclert A,
                                                                                                                                                                                                                                                                                                                                                           372
                                                                                                                                                                                                                                                               sequence tag;
mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identify mutations associated with a
                                                                                                                                                                                                                                                                                               EST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                           ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 341.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 G;
                                                                                                                                                                                                                                                                                               SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142
                                                                                                                       Giordano
                                                                                                                                                                                                                                                                                                NO: 3078.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                e tag (5' EST)
d to 5'ESTs and
ne mapping proc
                                                                                                                                                                                                                                                                          protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                377
                                                                                                                                                                                                                                                                                                                                                                                                             345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                s and for procedures
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sequence. The 5' ESTs were prepared from total human RNAs or polyA+ R derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they a often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of
                                                                                                                     mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5 UTR is rarely included. 5 ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
Sequence 372 BP;
                                                                                                gene therapy and chromosome mapping procedures. They
                                                                         upstream regulatory sequences and to design expression and secretion
  105
Α;
  87 C; 53 G;
  117 T;
  10 other;
                                                                                                     are used to obtain
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Matches
                                                                                                                                                                                                          Query Match
Best Local
 341
                300
                                 281
                                                 240
                                                                  221
                                                                                  180
                                                                                                   161
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                                                                                                                                   101
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        tggggctctgttttgttcattaattctggagc 331
                                         tggggctctgttttgttcattaattctggagc 372
                                 ttmaccttgtndaaaccatatccaaggtttccctttatatttctttcanratatccattc
                                                                  ttagggactatccagawcctgtttggaattatgnccttttcttttggagttatcttcctt
                                                                                                                                                                                                   321;
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                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                          46.3%;
96.7%;
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                                                                                                                                                                                                          Score 312.8;
Pred. No. 1.4
                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                   372;
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RESULT
AASO4280
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                                                                                                   CDS
                                                                                                                                                             Human; membrane protein; membrane receptor; IgE receptor;
physiological disorder; ss.
                                                                                                                                                            physiological
                                                                                                                                                                                                                                                                           AAS04280 standard;
12-DEC-2000; 2000WO-US33742
                          28-JUN-2001
                                                 WO200146417-A2
                                                                                                                                       Homo
                                                                                                                                                                                                                                                  AAS04280;
                                                                                                                                                                                                  Novel human
                                                                                                                                                                                                                          26-SEP-2001
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                                                                                                                                       sapiens.
                                                                                                                                                                                                membrane protein
                                                                                                                                                                                                                         (first entry)
                                                                        /product=
                                                                                    /*tag=
                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                           cDNA; 246
                                                                        "Human membrane protein
                                                                                                                                                                                                  #2
                                                                                                                                                                                                                                                                           ВР
                                                                                                                                                                                                cDNA sequence.
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CD20;

22-DEC-1999;

99US-0171567

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AAH64745
ID AAH6
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                                                                                                                                                                                                                           RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes for novel human membrane protein #2. Human membrane protein #2 is 1 of 4 human membrane proteins (AAU01210-AAU01213) given in the present invention. These membrane proteins share structural similarity with membrane receptors such as the IgE receptor and mammalian CD20. The novel human membrane proteins are useful for identifying agonists, antagonists and modulators of the membrane proteins, and for producing antibodies specific to the drug screening, harmacogenomic applications, clinical trial monitoring and the treatment of physiological disorders and diseases. The polynucleotides encoding the membrane proteins can be used to generate polynucleotides encoding the membrane proteins can be used to generate polynucleotides encoding the membrane proteins can be used to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identifying agonist, antibodies useful in
           WO200142451-A2
                                      Homo sapiens.
                                                                   GENSET;
                                                                                                             Human secreted
                                                                                                                                                                     AAH64745;
                                                                               Human;
                                                                                                                                       11-SEP-2001
                                                                                                                                                                                              AAH64745 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apprications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide encoding novel human membrane protein, useful for identifying agonist, antagonist or modifiers or for producing antibodies useful in therapeutic, diagnostic and pharmacogenomic
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nes 246; Conserv
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DB; AAU01211.
                                                                               secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.4%; ilarity 100.0%; Conservative
                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP;
                                                                                                           protein
                                                                            protein; gene therapy; vaccine; treatment; diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 A;
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                                                                                                           cDNA,
                                                                                                                                                                                                 468
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0; Mismatches
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                                                                                                           SEQ
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                                                                                                             NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
1.7e-57;
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RESULT
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AC AAF5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases associated with inappropriate GENSET gene expression. For cexample, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 230; Conserv
                                                 AAF58252 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 581; 921pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety or diseases, and for diagnosis of those diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-DEC-1999;
06-MAR-2000;
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DB; AAG89142.
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2000US-0187470
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Pred. No. 2.7e
0; Mismatches
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AAF58252

24-APR-2001

(first entry)

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17-MAR-2000;
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17-MAR-2000;
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ID AAF58254;
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XX Oligonucleotide D187
XX Electron-transfer gr
KW Electron-transfer gr
KW gene expression; ss.
OS Synthetic.
XX PD W0200107665-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide D1875
                                                                                                                                                                                                                                                                                                                                                          monitoring gene
                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CLIN-) CLINICAL MICRO SENSORS
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                                                                 ttaaaaccatatccaaggtttccctttatatttctttcaggatatccattctggggctct
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                                                                                                                                                                                   gtatttcctccagaaatcactgcttcagaatatgagtccacagaactttcagccacgacc
                                                                                                                                                                                                                                           Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                   936 BP; 4 A; 144 C; 7
                                                                                                                                                                                                                                                                        16.1%; Score 108.8; ilarity 0.7%; Pred. No. 5.1a Conservative 418; Mismatches
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2000US-0190259.
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.1e-20;
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                                                                                                                                                                                                                                                                                                                                   other;
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                                                                                                                                                                                                                                                                           Indels
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HORSE SERVICE 
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                                                                The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
  Sequence
                                            and single-nucleotide polymorphisms,
monitoring gene expression.
                                                                                                                                                                                                                                                                     Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping, a single surface
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                                                                                                                                                                                                              Example 6;
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Query Match Best Local Similarity

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                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to a composition comprising
                    gattgtgattgtgaacaatgttgttgactagcactgtgagaataaagatgtgttaaaata
                                                            ttcagcattattgaattattcatttctctgcctttctcaattttggggtgccactcagag
                                                                                                      aatagtcagtgtaaggctgttactgtcctgttcttgggaattttgattacattgatgact
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0.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 108.8;
Pred. No. 5.1
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Matches 5
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                                                                                                                                                                                                                                                                         Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
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gene expression; ss.
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                                                                                                                                                                                                                   y Match 16.1%; Score 108.8; DB 22; Local Similarity 0.7%; Pred. No. 5.1e-20; hes 5; Conservative 418; Mismatches 245;
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Search completed: November 29, 2001, 00:23:58 Job time: 4315 sec

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Minimum DB
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Perfect score:
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-07-869-933-22
US-09-103-663-22
US-08-724-394A-21
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1827.395 Million cell updates/sec
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Sequence 38, Appl	Sequence 48, Appl	Sequence 48, Appl	Sequence 8, Appli	Sequence 2, Appli	Sequence 89, Appl	Sequence 85, Appl	Sequence 1, Appli	Sequence 4, Appli	Sequence 11, Appl	Sequence 9, Appli	Sequence 81, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli

ALIGNMENTS

; LIBRARY: BRAII ; CLONE: 927955 US-08-916-902A-2 RESULT 1 US-08-916-902A-2 Sequence 2, Patent No. APPLICATION NUMBER: US/08/916 FILING DATE: Herewith CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-0 GENERAL INFORMATION: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: STREET: 31/7. STREET: 31/7. CITY: Palo Alto STATE: CA COUNTR: USA ZIP: 94304 ZIP: 94304 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible APPLICANT: Lal, preeti APPLICANT: COTley, Neil C. TITLE OF INVENTION: HIGH AFFINITY TITLE OF INVENTION: RECEPTOR-LIKE NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: STRANDEDNESS: TOPOLOGY: line IMMEDIATE SOURCE: TELEPHONE: 415-855-0555 APPLICANT: Bandman, Olga LENGTH: TELEFAX: 415-845-4166 ADDRESSEE: 2, Application 5. 5871930 nucleic acid E: Incyte Pharmaceuticals, Inc 3174 Porter Drive BRAINOT 04 linear single US/08916902A US/08/916,902A PF-0371 US IMMUNOGLOBULIN PROTEIN

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APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HIGH AFF
TITLE OF INVENTION: RECEPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application Patent No. 5977072
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Best Local Similarity
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              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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TELEPHONE:
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US-08-318-492-3
; Sequence 3, Application US/08318492
; Patent No. 5552312
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Best Local Similarity
Matches 232; Conserv
                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                             APPLICANT: Lim, Bing
APPLICANT: Adra, Chaker N.
APPLICANT: Lelias, Jean-Michel
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton,
                                                                                                                                                                                     TITLE OF INVENTION:
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LIBRARY: BRAINOTO4
CLONE: 927955
                                                                                                                                                                     NUMBER OF SEQUENCES:
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LENGTH: 1669 base pairs
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Pred. No. 6.1e-15;
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                                                                                                Sequence 3, Application US/08707340 Patent No. 5705615 GENERAL INFORMATION:
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Best Local Similarity
Matches 239; Conserv
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NAME: BIOOK, DAVID E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: BIH9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
            APPLICANT: Lim, Bing
APPLICANT: Adra, Chaker N.
APPLICANT: Lelias, Jean-Michel
TITLE OF INVENTION: RECOMBINANT HTM4 GENE, PROTEIN
TITLE OF INVENTION: ASSAYS
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NUMBER OF SEQUENCES:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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US-08-707-340-3
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Best Local Similarity
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FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/675
FILING DATE: 03-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYOOK DAVID E.
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: BH99
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-9340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Kelec
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE: 03-SEP-199)
CLASSIFICATION: 536
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OPERATING SYSTEM:
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COUNTRY:
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SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                 FEATURE:
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APPLICATION NUMBER:
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APPLICANT: Adra, Chaker N.
APPLICANT: Lelias, Jean-Mi
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                                                            294 TGTCTTTCTGGGTTCCTTGCAATACCCATACCACTTCCAAAAGCACTTCTTTTTTCTTCAC 353
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LOCATION:
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                                                                                                                                Local Similarity
nes 239; Conserv
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Brook, David E.
Brook, David E.
22,592
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Two Militia Drive
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                                                                                                                               Score 63.2; DB 2;
Pred. No. 1.7e-08;
0; Mismatches 213;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                       TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
                                         FEATURE:
                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2545 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
                                                                                                    FEATURE:
                                                                                                                    MOLECULE TYPE:
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NAME/KEY:
LOCATION:
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FILING DATE: 19920416
CLASSIFICATION: 514
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TELEFAX: (703)683-4109
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1800 Diagonal Road,
  sig_peptide
                                                          46..786
                                                                                                                    CDNA
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: ISOLATION, CHARACTERIZATION, AND USE OF
: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
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US-07-869-933-22

NAME/KEY: LOCATION:

mat_peptide 55..786

Length 2545;

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; LOCATION: (46)..(786)
US-09-103-663-22
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US-09-103-663-22
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APPLICANT: Kinet et al.
APPLICANT: Kinet et al.
TITLE OF INVENTION: Isolation, characterization, and use of the human beta
TITLE OF INVENTION: subunit of the high affinity receptor for
TITLE OF INVENTION: immunoglobulin E.
FILE REFERENCE: 50490
                                                                                                                                      Best
                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 158;
                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 22
LENGTH: 2545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/09103663D Patent No. 6171803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/103,663D CURRENT FILING DATE: 1998-06-23 EARLIER APPLICATION NUMBER: 07/869,933
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1992-04-16
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                  NAME/KEY: sig_peptide LOCATION: (46)..(54)
                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                   193
                                                    188
                                                                     133 caactcaaagccccttgcaaaaattatttgctagaaaaatgaaaatcttagggactatcc 192
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                                                                                                                                    Local Similarity
agatcctgtttggaattatgaccttttcttttggagttatcttccttttcacctt-----
                                                caccacagcagacatggcagtcatttttgaagaaagagttggagttcctgggcgtaaccc 247
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                                                                                                                                    Score 49.2; DB 4;
Pred. No. 0.00015;
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Pred. No. 0.00015;
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                                                                                                                     Mismatches
                                                                                                                     138;
                                                                                                                                                 Length 2545;
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Query Match
Best Local Similarity 6.6%
27; Conservative
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Patent No. 5
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMPLECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                            TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                            IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
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                                                                                                                                                                                                                                                          (703)683-4109
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                                                                                                                                              linear
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                                                                                                                                                             single
             6.3%; Score 42.6; DB 6.6%; Pred. No. 0.015; ative 204; Mismatches
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RESULT 9
US-08-724-394A-20
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                                                             TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                 CLASSIFICATION: 536
ATTOREY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Megabase .
TITLE OF INVENTION: Sequences
TITLE OF INVENTION: 31
                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Wolff, Roger K.
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                                                                                                                                                                                                                                     APPLICATION NUMBER: US/01 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
              STRANDEDNESS:
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                                              ENGTH:
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                         : 246240 base pairs nucleic acid
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Lauer, Peter M.
Ruddy, David A.
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not relevant
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Sequences and Antibodies
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Best Local Similarity
Matches 67; Conserv
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                                                                                                                  TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
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                                           MOLECULE TYPE:
                                                                                                                                                                  TELEPHONE: 415-576-0200
                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/724,394A FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
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                              FEATURE:
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: YWO LANCE CITY: San Francisco
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                           TOPOLOGY:
                                                                         STRANDEDNESS:
                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                      246240 base pairs
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Wolff, Roger K.
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Sequences and Antibodies Thereto
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/note= "HLA-H.CONTIG"

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; LOCATION: 1..2462;
; OTHER INFORMATION:
US-08-724-394A-22
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CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
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APPLICANT:
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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
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CURRENT APPLICATION DATA:
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                                                                                MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                            NAME/KEY: misc_feature
                                                                                                           STRANDEDNESS:
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Wolff, Roger K.
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Sequences and Antibodies Thereto
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               /note= "HLA-H.CONTIG"
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; LOCATION: US-08-568-147B-1
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Best Local Similarity
Matches 67; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                        APPLICATION NUMBER: 800, FILING DATE: 02-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,
                                 FEATURE:
NAME/KEY:
                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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STATE: New York
                                                                               STRANDEDNESS: bo
TOPOLOGY: · linear
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 84
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                                                                                                             TYPE: nucleic acid
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VENTION: DNA FRAGMENT CODING FOR SQUAMOUS CELL
VENTION: CARCINOMA-ASSOCIATED ANTIGEN
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                62..1234
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Pred. No. 9.2;
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Query Match . 5.0%; Best Local Similarity 47.6%; Matches 99; Conservative

Score 33.6; DB 1; Length 1711; Pred. No. 2.7;

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LOCATION: (3677)...(3951)
OTHER INFORMATION: n can be any nucleotide
US-09-212-971-5
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US-08-800-929A-5/c; Sequence 5, Appl
                                         RESULT
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Best Local Similarity
Matches 70; Conserv
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LENGTH: 6669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/30,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND TITLE OF INVENTION: MAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE TITLE OF INVENTION: DISEASE FILE REFERENCE: 07891/009002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1997-02-13
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APPLICANT: MacKenzie, Alexando
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APPLICANT: Pratt, Christine
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APPLICANT: Baird, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                    2826 ATGTTTCTGAA
                                                                                                                                                                                                                                                            2946 TGGCTGTAAAATAAGACCTTTCAAAGATTTTAAAATTTTTTGTCCCCCTCAAAGAACTAAC 2887
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Application US/08800929A
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SEQUENCE CHARACTERISTICS:
LENGTH: 6669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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GENERAL INFORMATION:
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FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bleker-Brady, Kristina
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APPLICANT:
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                                                                                                                                        2946 TGGCTGTAAAATAAGACCTTTCAAAGATTTTAAATTTTTTTGTCCCCCTCAAAGAACTAAC 2887
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
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2826 ATGTTTCTGAA 2816
                                                                     2886 ATTGTAGAGTTATTCAACTTATCACCTCCTGAAAACATTTTTGAACTTTTGTTTTTTCTAA 2827
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                                                                                                                                                           160 ttgctagaaaaatgaaaatcttagggactatccagatcctgtttggaattatgacctttt 219
                                280 ttctttcagga 290
                                                                                         220 cttttggagttatcttcctttttcaccttgttaaaaccatatccaaggtttccctttatat 279
                                                                                                                                                                                                                          Watch 4.9%; Local Similarity 53.4%;
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OPERATING SYSTEM:
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STATE: MA
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RESULT 15 US-09-617-053A-5/c ; Sequence 5, Application US/09617053A ; Patent No. 6300492 ; GENERAL INFORMATION:

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Search completed: November 29, 2001, 00:23:11 Job time: 9823 sec
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                                          2826 ATGTTTCTGAA 2816
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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AA758635 ah67b04.s
BEI07659 UI R-BF1-
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REFERENCE AUTHORS TITLE SOURCE ORGANISM RESULT 1 AI149899/c LOCUS VERSION KEYWORDS COMMENT FEATURES ACCESSION DEFINITION JOURNAL source ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 742 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 455. Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov mRNA sequence. AI149899 AI149899.1 GI:3678368 AI149899 508 bp mRNA EST 10-NOV-1998 qf43h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752827 s.milar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20 ;, cDNA Library Preparation: M. Bento Soares, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anat human: (bases 1 to 508) /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1752827" Location/Qualifiers . 508 Anatomy Project (CGAP), Ph.D., **.** Fatima Bonaldo

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Hillier,L.,
          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 516)
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zu03a08.rl Soares_testis_NHT Homo sapiens cDNA clone
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/sex="male"
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Allen, M.,
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Pred. No. 4.3e-102;
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Bowles, L.,
                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
Dubuque, T.,
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                                            CAGAAACTCTGATAATATTGAGCCGAATAATGAATTTTCTTAGTGCCCTGGGAGCAATAG
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Location/Qualifiers
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Fax: 314 286 1810
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4444 Forest Park Parkway,
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Steptoe,M., Tan,F., Theising,B.,
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AA416972
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3. similar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20
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Contact: Wilson RK
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Krizman,D., Kucaba,T., Lacy,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer: -41m13 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                   138
                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                             (Pharmacia), digested with Not I and cloned into the Not I and Econed into the Not I sand Econe into the Not I was constructed by Bento Soares and M. Fatima Bonaldo. " 77 c 67 g 105 t
                                                                                                                                                                                                                                                                                                                                               /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:730041"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:5926570"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
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98.7%;
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                                                                                                                                                                             Score 379; DB 10
Pred. No. 2e-74;
                                                                                                                                                                 Mismatches
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                                                                                                                                                                                               Length 387;
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actgtgagaataaagatgtgttaaaaat 667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White,Y., Wylie,T., WashU-NCI human EST Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA435988 382 bp mrNA 109-NOV-1997 zu03a08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730742 3' similar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20;
                                                                                                                                                                                                                                                                                                                                                                                                                     Possible reversed clone: similarity Insert Length: 733 Std Error: 0.00 Seq primer: -41n13 fwd. ET from Amer High quality sequence stop: 280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4444 Forest Park Parkway, Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
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          135
/organism="Homo sapiens"
/db_xref="GDB:5927437"
                                                                                                                                                                                                                                    /lab_host="DH10B"
                                                                                                                                                                                                                                                          /sex="male"
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AA758635
AA758635.1
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ah67b04.sl
similar to
                                                                                         www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 661 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 390
                                                                                                                                               CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M.
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 394)
                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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milarity 99.0%;
Conservative
           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1320655"
/clone_lib="Soares_testis_NHT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                    394 bp mRNA EST 29-DEC-1996 Soares_testis_NHT Homo sapiens cDNA clone 1320655 SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20 ;,
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                                                                               on/Qualifiers
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637 tagcactgtgagaataaagatgtgttaaaaataaa
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                                                                                                                                                                                                                                                                                   tycaytyaaaayaaaaccacayaaactctyataatattyayccyaataatyaatcttct 400
TAGCACTGTGAGAATAAAGATATGTTAAAATAAA
                                                                   gccttt-ctcaattttggggtgccactcagaggattgtgattgtgaacaatgttgttgac 636
                                                                                                                                                                                                                                tagtgccctgagagcaatagctggaatcattctcctcacatttg-gtttcatcctagatc 459
                                                                                                                                                                                                                                                                     TGCAGTGAAAAGAAAACCACAGAAACTCTGATAATATTGAGCCGAATAATGAATTTTCT 275
                                                    GCCTTTACTCAATTTTGGGGTGCCACTCAGAGGATTGTGATTGTGAACAATGTAGTTGAC
                                                                                                                                                           AAAACTACATTTGTGATTATTCTCACCAAAATAGTCAGTGTAAGGCTGTTACTGTCCTGA 155
                                                                                                                                                                                                                TAGTGCCCTGGGAGCAATAGCTGGAATCATTCTCATCACATTTGAGTTTCATCCTAGATC 215
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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95.7%;
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                                                                                                                                                                                                                                                                                                                                                                                             Score 325.2; DB 1
Pred. No. 1.8e-62;
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                           670
                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Length 394;
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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                  BE107659 484 bp mRNA EST UI-R-BT1-ame-d-04-0-UI.S1 UI-R-BT1 Rattus norvegicus UI-R-BT1-ame-d-04-0-UI 3', mRNA sequence.
                                                                                                                                                                               Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr
                                                                                                                               97044477
                                                                                                                                                  Genome
                                                                                                                                                                  discovery
                                                                                                                                                                                                                                        Rattus
                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                            Rattus
                                                                                                                                                                                                                                                                                                               Norway rat
                                                                                                                                                                                                                                                                                                                                                   BE107659.1
                                                                                                                                                                                                                                                                                                                                                                      BE107659
Email: msoares@blue.weeg.uiowa
                                                                                                                                                                                                                   (bases 1 to 484)
                                                                                                                                               Res. 6 (9),
                                                                                                                                                                                                                                                                                            norvegicus
                                                                                                                                                                                                                                                                                                                                                   GI:8499769
                                                                                                                                             791-806 (1996)
                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 agateetgttttggaattatgaeettttettttggagttatetteetttteacettgttaa 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   taatattgagccgaataatgaatcttcttagtgccctgagagcaatagctggaatcattc 432
aaaa 676
                                                                                                                                                                                                                                                                                                                                gtcagtgtaaggctgttactgtcctgttcttgggaattttgattacattgatgactttca 552
                                                                                        gtgattgtgaacaatgttgttgactagcactgtgagaataaagatgtgtttaaaataaaaa 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaccatatccaaggtttccctttatatttctttcaggatatccattctggggctctgttt 312
                                                                                                                                                                                GCGTTGCTGAACTGTTCATTTCCCTCTTTTCCTCGATTTTGGGGTGCTACTCAGAAGAAA 65
                                                                                                                                                                                                         gcattattgaattattctcttgtgttttttctcaattttggggtgccactcagaggatt 612
                                                                                                                                                                                                                                                                                                 TTCAGTGTGGTGCTATTACCACTCTATTTGTTGGGATTTTGATTATGTTGATGATCTTCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                        tcctcacatttggtttcatcctagatcaaaactacatttgtggttattcttcaccaaaata 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGATCCTGTTTGGAATCATGAACTTCTCATTTTGGAGTTGTTTTCCCTTTTTCACCTTGGTAA 425
                                                                                                                                                                                                                                                                                                                                                                                                                        TCCTCATATGTGCTTTCCTTCTAGATGGAGAATTCATCTGTGGCTATTCTCCAGATGGTA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics (www.resgen.com)
Seg primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized testis library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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/note="Vector: pT/T3D-Pac (Pharmacia) with a modified note: Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The library UI-R-BFI is a subtracted library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously accepted to the company of the library from which this clone was derived, please visit our web site at the subtraction has been previously accepted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG_SEQ=ACGCAG"
98 c 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_LIB=UI-R-BT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  described in (Bonaldo, Lennon and Soares, Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BT1 - ame-d-04-0-UI"
/clone_lib="UI-R-BT1"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAG_TISSUE=testis
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                                                        ATGCTGTTGAATAGCACTGTACAAGTAAAACTGCAAATTGAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.38;
76.98;
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Matches 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                CCACGACCTTTTCAACTCAAAGCCCCCTTGCAAAAATTATTTGCTAGAAAAATGAAAATCT 204
           ccacgaccttttcaactcaaagccccttgcaaaaattatttgctagaaaaattgaaaaatct 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAA
                                                 TGTTTCTGGTATTTCCTCCAGAAATCACTGCTTCAGAATATGAGTCCACAGAACTTTCAG 144
                                                             tgtttctggtatttcctccagaaatcactgcttcagaatatgagtccacagaactttcag 120
                                                                                                                                                    389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White, Y., Wylle, T., Waterston, R. and Wilson, R. Tanier, D., Washu-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA470059 415 bp mRNA EST 09-NOV-1997 zt94h05.rl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730041 5' similar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
1 (bases 1 to 415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                               Similarity
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                                                                                                                                                                                                                               129
                                                                                                                                                    Conservative
                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:5926570"
/db_xref="taxon:9606"
/clone="IMAGE:730041"
                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
                                                                                                                                                             40.7%;
                                                                                                                                                   Score 274.8;
Pred. No. 2.96
0; Mismatches
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2.9e-51;
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ot38b02.s1 Soares_testis_NHT
3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominiu.
1 (bases 1 to 482)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3', mRNA sequence.
AI002083
                                                                                                                                                                                                                                                                                       www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
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                                                                                                                                                                                                                                                                          Insert Length:
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                                                                                                                                                                                                                                                                                                                                                                         Library Preparation:
/sex="male"
                                                                                                                                                                             /clone="IMAGE:1619019"
                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                         /organism="Homo sapiens"
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482; Conservative
                              Eukaryota;
Mammalia; E
                                                                                                             AA411806 410 bp mRNA
zt67a03.sl Soares_testis_NHT
zt67a03.sl Soares_testis_NHT
        Hillier, L.,
                                                                                                     mRNA sequence.
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                  karyota; Metazoa;
mmalia; Eutheria;
(bases 1 to 410)
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         Allen, M.,
                                                                                  GI:2070377
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          Bowles, L.,
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 Lennon, G.,
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T Homo sapiens cDNA clone
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Dubuque,T., Genn,G., Marra,M.,
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          Geisel, G.,
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Martin, J.,
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          Jost
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                                      sequence.
                                                                  ai58g01.s1
similar to
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 608 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
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WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
                                                                                              AA781801
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Location/Qualifiers
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:5924284"
/db_xref="taxon:9606"
/clone="IMAGE:727372"
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                                                                 389 bp mRNA
Soares_testis_NHT Homo
SW:CD20_HUMAN P11836 B-
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96.1%;
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Pred. No. 1.3e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          252;
AQ108532
                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anat
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/db_xref="taxon:9606"
/clone="1375056"
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/sex="male"
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95.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 245.4; DB Pred. No. 1e-44; O; Mismatches
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clone 2379G7,
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                                                                                                                                                                                                                                                                                                                                                                                                              212 ATTCATTTCTCTGCCTTTCTCAATTTTGGGGTGCCACTCAGAGGATTGTGATTGTGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Sin
hes 154;
                                                                                                                                                                                                                                                                                                                                                                  attcatttctctgcctttctcaattttggggtgccactcagaggattgtgattgtgaaca 625
                                                                                                                                                                                                                                                                                      ATGTTGTTGACTAGCACTGTGAGAATAAAGATGTGTTAAAATA 314
           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                           Mammalia; Eutheria;
1 (bases 1 to 281)
                                                                          Homo sapiens
Eukaryota; Metazoa;
                                                                                                                              EST
                                                                                                                                           AA707529.1
                                                                                                                                                           AA707529
                                                                                                                                                                          mRNA sequence.
                                                                                                                                                                                        AA707529 281 bp mRNA E9 ah41a12.s1 Soares_testis_NHT Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mdadams@tigr.org
Clones are available from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ108532.1
GSS.
                                                                                                             human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of a random human BAC End Sequence Database for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter, J.C.
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1 (bases 1 to 538)
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301 838 0208
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Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2379G7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="CIT-HSP"
/sex="Male"
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                                                                                                                                            GI:2717447
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Primates;
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Primates;
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Pred. No. 3.3e-23;
Pred. No. 3.3e-23;
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                                                          Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                            Vertebrata;
             Anatomy Project (CGAP),
                                                           Hominidae;
                                                                                                                                                                                         cDNA clone
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one 1292062 3',
                                                                            Euteleostomi;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                           TGTGAGAATAAAGATGTGTTAAAATAAA 1
Mammalia; Eutheria; Rodentia; Sciurognathi; Murldae; Murinae; Mus. 1 (bases 1 to 332)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                   uy63h11.x1 McCarrey Eddy round spermatid Mus musculus cDNA clone IMAGE:3664293 3', mRNA sequence.
                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                        BF319786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 456 Std Error: 0.00
                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                       BF319786.1 GI:11268601
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
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/db_xref="taxon:9606"
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                                                                                                                                                                              Metazoa;
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                                                                                                                                                                                                                                                                                                                    332 bp
                                                                                                                                                              Chordata;
Rodentia;
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Pred. No. 5.2e-23;
0; Mismatches 0;
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                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 281;
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                                                                                                                                                                                                                                                                                                                                              GCAGTGTGGTGTTATTACCATTCTATTCATTGGGATTTTGGTTATGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTCATATTTGGCTTCCTAGATGGGGAATTCATCTGTGGCTATTCTCCAGATGGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174;
                                                                                                                                             EST 28-AUG-200 LSTUUUU3 mouse testis apoptosis subtraction cDNA library Mus musculus cDNA clone MTA03 5', mRNA sequence.
Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                           BE638317.1 GI:9932060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 313.
                                                                              house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single-stranded phagemids were prepped and tranformed into DB10B. Library contains 98.5% recombinants. References: J. Androl. 20:635-639 and Gene 25:263-269. Library constructed and donated by J. McCarrey, Ph.D. (Southwest Foundation for Blomedical Research, Dept. of Genetics); excision done by E.M. Eddy, Ph.D. (National Institutes of Health, National Institute of Environmental Health Sciences). Original lambda-based library is available through ATCC, catalog #63423."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pBluescript SK+ (Stratagene /note="Torgan: testis; Vector: pBluescript SK+ (Stratagene ); Site_1: XhoII: Site_2: EcoRI; cDNA oligo dT-primed (5'-(GA)10-ACTAGTCTCGAGTTTTTTTTTTTTT-3') and directionally cloned using 5' linkers 5'-AATTCGGCACGAG-3' and 5'-CTCGTGCCG-3'. Size selection of >4000 material gives average insert size ranging from 1-2 kb. Library was mass excised (from lambda-UnizAP-XR) and resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="round spermatids, pooled from multiple mice"
/dev_stage="60 day"
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/clone="IMAGE:3664293"
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76.0%;
  Chordata;
Rodentia;
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Pred. No. 1.8e-21;
0; Mismatches 55;
  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169;
                            Unpublished (2000)
Contact: Jiang H
                                                                                                                                                                                               EST00022 mouse testis apoptosis subtraction musculus cDNA clone MTA22 5', mRNA sequence. BE638325 BE638325.1 GI:9932068
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88 Xiangya road, Changsha, Hunan 410078, China
Tel: 086-0731-4897661
Fax: 086-0731-4497661
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Unpublished (2000)
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                                                           cDNA library
                                                                         Jiang, H., Li, L. and Expressed sequence
                                                                                                       Mammalia; Eutheria;
1 (bases 1 to 224)
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Seq primer: T7 Promoter Primer
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medical University
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158 c 146 g
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177 atcttagggactatccagatcctgtttggaattatgaccttttctttttggagttatcttc 236
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                                                                     ATCTTAGGGACCACCCAGATCCTGTTTGGAATCATGAACTTTTCATTTGGAGTCATTTTC 25
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Tel: 086-0731-4805036
Fax: 086-0731-4497661
Email: 1j12@public.cs.hn.cn
Seq primer: T7 Promoter Primer
High quality sequence stop: 224.
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/lab_host="JM109"
/note="Vector: pUCm-T"
40 c 61 g 65 t
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Search completed: November 29, 2001, 00:18:44 b time: 9881 sec

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Listing first 45 summaries
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  November 28, 2001, 21:32:37; Search time 1789.67 Seconds (without alignments) 4148.100 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	RESULT 1 AX179787 LOCUS DEFINITION ACCESSION VERSION	CC C CC 222 222 222 222 222 222 222 222	. 128456789012845678c	Result
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                                                                                                                       Human membrane proteins and polynucleotides encoding the having homology to cd20 proteins and ige receptors Patent: Wo 0146417-A 1 28-JUN-2001; Lexicon Genetics Incorporated (US)
                                                                                                                                                                         Eukaryota; Metazoa; Chorda
Mammalia; Eutheria; Primat
1 (bases 1 to 603)
Walke,D.W. and Turner,C.A.
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                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
125 c 104 g 21
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94 c 77 g
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Primates;
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                           Score 347.4; DB 6;
Pred. No. 2.5e-67;
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Pred. No. 4.7e-90;
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                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 676) Walke, D.W. and Turner, C.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (20-APR-1998) Kenichi Ishibashi, Tokyo Medical and University, 2nd Internal Medicine; Yushima 1-5-45, Bunkyo, Tc 113-8519, Japan (E-mail:kishibashi.med2@med.tmd.ac.jp, Tel:81-3-5803-5223, Fax:81-3-5803-0132)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishibashi,K., Sasaki,S
Cloning of three CD20
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 (bases 1 to 691) Ishibashi, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens mRNA
AB013103
AB013103.1 GI:115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens testis cDNA to
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/db_xref="taxon:9606"
/tissue_type="testis"
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ee CD20 homolog from
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Identification of a cd20-, fcepsilonribeta-, family: sixteen new ms4a family members expre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (24-FEB-2000) Immunology,
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mmalia; Eutheria; Primates;
(bases 1 to 694)
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1 (bases 1 to 697)

Hulett, M.D., Pagler, E., Hornby, J.R., Hogarth, P.M., Eyre, H.J., Baker, E., Crawford, J., Sutherland, G.R., Ohms, S.J. and Parish, C.R. Isolation, tissue distribution, and chromosomal localization of a novel testis-specific human four-transmembrane gene related to CD20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete
AF321127
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accttttcttttggagttatcttccttttcaccttgttaaaaccatatccaaggtttccc
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                                                                                                                   tcagaatatgagtccacagaactttcagccacgacctttcaactcaaagccccttgcaa 120
                                              AAATTATTTGCTAGAAAAATGAAAATCTTAGGGACTATCCAGATCCTGTTTGGAATTATG
                                                                                                     TCAGAATATGAGTCCACAGAACTTTCAGCCACGACCTTTTCAACTCAAAGCCCCTTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            accttttcttttggagttatcttccttttcaccttgttaaaaccatatccaaggtttccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aaattatttgctagaaaaatgaaaatcttagggactatccagatcctgtttggaattatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5
AX179785
AX179785.1
                                                                                                                                                                                                                                                                                                                                                          Human membrane proteins and polynucleotides encoding having homology to cd20 proteins and ige receptors Patent: WO 0146417-A 5 28-JUN-2001; Lexicon Genetics Incorporated (US)
Location/Qualifiers
1. 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primat 1 (bases 1 to 417)
Walke, D.W. and Turner, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
91 c 69 g 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 bp DNA
Patent WO0146417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Primates;
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                                                                                                                                                                                                                         Score 340.8; DB 6;
Pred. No. 7.2e-66;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grant, G., Tilev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meddrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Marchan, C., Marchan, C., Mill, J., There's Marchan, A., Talamas, J., There's Marchan, C., Talamas, J., Tal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA (02141, USA On Aug 18, 2000 this sequence version replaced gi:7382629.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome Unpublished
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Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 15, clone RP11-196E16
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NOTE: This record contains 163 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
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                                                                                                                                                                    Center project name: L9008
Center clone name: 196_E_16
                                                                                                                                                                                                                                                                                                                Web
                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center
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                                                                                                                                                                                                                                     Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                http://www-seq.wi.mit.edu
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Barna,N., Bastien,V., Beda,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A HTG 18-AUG-2000 clone RP11-196E16 map 15, LOW-PASS
                                                                                                                                                                                                                                                                                                                                                                                    for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gage, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360
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* will be sequenced to completion. In the event th
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * arbitrary. Low-pass sequence sampling is useful for tidentifying clones that may be gene-rich and allows to verlap relationships among clones to be deduced. * overlap relationships among clones to be deduced. * However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved.
                                                                                                                                                                                                                                                                              1390 13489: gap of 100 bp 13490 14186: contig of 697 bp 14187 14286: gap of 100 bp 14287 14996: contig of 710 bp 14297 15096: gap of 100 bp 15797 15896: gap of 100 bp 15897 15883: contig of 687 bp 15884 16683: gap of 100 bp 1
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8733 9430: contig of 698 b
9431 9530: gap of 100 bp
9531 10214: contig of 684 b
0215 10114.
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7838 7937: gap of 100 bp
1938 8632: contin cf
633 p770
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3 3820: contin 100
1 3 100
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0234: contig of 711 k
6334: gap of 100
7040
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5423: contig of 697 l
5523: gap of 100 bp
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3042: co
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100 bp
140: contig of 706 k
140: gap of jnn 1837: conti
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18962: contig of 684 bp
9062: gap of 100 bp
19673: contig of 611 bp
                                                                                                                                                                                                                                                                                                                                                                                                       0314: gap of 100 bp
10980: contig of 666 bp
1080: gap of 100 bp
11783: contig of 703 bp
1883: gap of 100 bp
12582: contig of 699 bp
2512
290: gap or
25981: contig of
                                                           24391: cont
                                                                                 23595: cont
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536: gap of 100 b
21233: contig of 697
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4626: con
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22042: contig of 709
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20436: contig
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22808: contig
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17376: contig of 693 b
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18178: contig of 702
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* NOTE: This record contains 163 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (01-APR-2000) Whitehead Institute/MIT Center for Submitted, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 18, 2000 this sequence version replaced gi:7382629 All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches 6;
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and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preserved.
                                                                                                      22809
                                                                                                                                                                                                                                                                                                                                                                                                                   13390 13489: gap of 1
13490 14186: contig of 1
14187 14286: gap of 1
14287 14996: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp
10981 11080: contig of 666 bp in 1
10981 11080: gap of 100 bp
1081 11783: contig of 703 bp in 16
784 11883: gap of 100 bp
184 12582: contig of 699 bp in 1e
183 12682: gap of 100 bp
13389: contig of 699 bp in 1e
100 bp
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                                                   97 15996: contig of 700 bp in 16
97 15896: gap of 100 bp
97 16583: yap of 100 bp
984 16683: yap of 100 bp
114746: gap of 100 bp in 16
77 18178: contig of 693 bp in 16
77 18178: contig of 693 bp in 16
79 18278: gap of 100 bp
19962: contig of 684 bp in 16
63 19062: gap of 100 bp
63 19063: contig of 611 bp in 16
64 19773: gap of 100 bp
74 20436: contig of 63 bp in 16
75 21233: contig of 63 bp in 16
76 133: gap of 100 bp
37 21233: contig of 697 bp in 16
38 22108: contig of 697 bp in 16
39 22908: gap of 100 bp
43 22102: contig of 666 bp in 16
43 22102: contig of 666 bp in 16
43 22103: contig of 667 bp
65 23695: gap of 100 bp
67 24491: contig of 686 bp in 16
68 24491: contig of 686 bp in 16
69 24491: contig of 686 bp in 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 8632: contig of 6

33 8732: gap of 100

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31 9530: gap of 100

31 10214: contig of 6

15 10314: gap of 10

15 10316: contig of 6
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14 5523: gap of 10
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TOURNAL REFERENCE
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AUTHORS
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AC015840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baldwin, J., Barna, N., Beckerly, R., Boyuslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Maddrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Pollara, V., Timmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tcagaatatgagtccacagaactttcagccacgaccttttcaactcaaagccccttgcaa 120
                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 27, 2000 this sequence version replaced gi:6446828. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 147788)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 147788)
Birren, B., Linton, L., 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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Insert size: 203000; agarose-fp
Insert size: 147388; sum-of-contigs
Ouality coverage: 5.2 in Q20 bases;
                                                                     Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 136347 bases at least Q40 Consensus quality: 143600 bases at least Q30 Consensus quality: 146212 bases at least Q20 Consensus quality: 146212 bases at least Q20
                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                           Center clone name: 24_D_
                                                                                                                                                                                                                                                                Center project name: L4434
                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                            Center code: WIBR
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96.38;
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Pred. No. 2.8
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aaattatttgctagaaaaatgaaaatcttagggactatccaga 163
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 161039)
                                                                                                                                                                                                            AP003127 161039 bp DNA HTG
Homo sapiens chromosome 11 clone RP11-710G6
SEQUENCE, 15 unordered pieces.
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6595 6694; gap of 100 bp
6695 16187: contig of 9493 bp in length
16188 16287: gap of 100 bp
16288 25089: contig of 8802 bp in length
25090 25189: gap of 100 bp
25190 63923: contig of 38734 bp in length
63924 64033: gap of 100 bp
64024 147788: contig of 83765 bp in length
Location/Qualifiers
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Pred. No. 2.8e-24;
0; Mismatches 6;
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Consensus quality: 157456 bases at least Q40
Consensus quality: 158960 bases at least Q30
Consensus quality: 159457 bases at least Q20
Insert size: 159639; sum-of-contigs
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Center clone name: RP11-71066
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
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Contact: hattori@gsc.riken.go.jp
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149023 154159: contig of 5
154160 154259: gap of 1
154260 157686: contig of 3
157687 157786: gap of 1
157687 159234: contig of 1
159235 159334: gap of 1
159235 159334: gap of 1
159335 161039: contig of 1
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157787. .159234
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/note="assembly
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137320. .14327
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/db_xref="taxon:9606"
/chromosome="11"
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159335. .161039
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115803. .125183
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148922: contig of 5546 bp
149022: gap of 100 bp
154159: contig of 5137 bp
154259: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                           as soon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
On Nov 14, 2000 this sequence version replaced gi:8117704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (06-JAN-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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1 (bases 1 to 166804)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 166,804 genomic DNA of 11q12

Published Only in DataBase (2000) In press

2 (bases 1 to 166804)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Consensus quality: 162254 bases at least Q40 consensus quality: 163858 bases at least Q20 consensus quality: 164244 bases at least Q20 consensus quality: 164544 bases at least Q20 Insert size: 165004; sum-of-contigs Quality coverage: 9.28x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of Assembly program: Phrap; version 0.990329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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156020 159504:

159505 159604:

159605 159679:

159680 159779:

159680 159779:

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162419 165518:

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/note="assembly_fragment" 140526. .144653
                                                                 /note="assembl
126403. .13347
                                                                                                                                                                  93819.
                                /note="assembly_fragment"
133580. .140425
                                                                                                /note="assemb]
117107. .1263(
                                                                                                                                 108158
                                                                                                                                             /note="assembly_fragment"
                                                                                                                                                                                                  77680.
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                                                                                                                                                                                                                                   64379.
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/chromosome="11"
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                                                                                                                                   .117006
                                                                   .133479
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                                                                               y_fragment"
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1 2398: contig of 2398 bp in length
22399 22498: gap of 100 bp
45239 45238: contig of 22740 bp in length
45239 45338: gap of 100 bp
45339 64278: contig of 18940 bp in length
64279 64378: gap of 100 bp
64279 64378: gap of 100 bp
77579: contig of 13201 bp in length
77580 77679: gap of 100 bp
77680 93718: contig of 16039 bp in length
93819 93818: gap of 100 bp
108057: contig of 16039 bp in length
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                                                                                                                                                                                                                                                                                                                                                                               108058 108157: gap of 100 to 108158 117006: contig of 8849
                                                                                                                                                                                                                                                                                                 .33480 133579: gap of .33580 140425: cont
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                       Location/Qualifiers
organism-"Homo sapiens"
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14752
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945/
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4622: gap of 100 |
155919: contig of 1297
                                         5483: gap of
166804: cont
                                                                    2518: gap of
165383: cont
                                                                                        3779: gap of 100 b
162418: contig of 2639
                                                                                                                                      gap of
                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                    contig of 7077 bp
                                                                 contig of 2865
                                                                                                                                                                                                                                     contig of 4601
                                                                                                                                                                                                                                                                   ap of 100 bp contig of 4128 bp
                                                                                                                                                                                                                                                                                                                                                     contig of 9196
                                        contig of 1321
                                                                                                                      contig of 75 bp
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
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                                 Birren B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barra, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illey, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., MacGonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Mylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schughack, R., Seaman, S., Severy, P., Soughack, R., Seaman, S., Severy, P., Soughack, R., Seaman, S., Severy, P., Soughack, R., Seaman, S., Severy, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tcagaatatgagtccacagaactttcagccacgaccttttcaactcaaagccccttgcaa 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 11, clone RP11-729B4
    Sougnez,C.,
Strauss,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 11 clone SEQUENCE, 2 ordered pieces.
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154623. .15591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
165484. .166804
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159780. .162418
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159605, .159679
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156020. .159504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment"
162519. .165383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa; Chordata; Craniata; Vertebrata;
Butheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166820 bp
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                       Spencer, B., Stange-Thomann, N., Stojanovic,
    Subramanian, A.,
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96.3%;
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Tesfaye, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae;
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                                          61 tcagaatatgagtccacagaactttcagccacgaccttttcaactcaaagccccttgcaa 120
                                                                                                                                                                                                                 Local Similarity
                                                                                                                  1 atggattcaagcaccgcacacagtccggtgtttctggtatttcctccagaaatcactgct 60
                                                                                                                                                                                        157;
ATGGATTCAAGCACCGCACACAGTCCGGTGTTTCTGGTATTTCCTCCAGAAATCACTGCT 144041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 20, 2001 this sequence version replaced gi:12958037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zembek, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 166378 bases at least Q40 Consensus quality: 166639 bases at least Q30 Consensus quality: 166692 bases at least Q30 Consensus quality: 166692 bases at least Q20 Insert size: 176000; agarose fp Ouality coverage: 12.2 in Q20 bases; agarose-fp Quality coverage: 12.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the accession number will be preserved.

1 1095: contig of 1095 bp in length
1096 1195: gap of 100 bp
1196 166820: contig of 165625 bp in leng-
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Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hon Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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15 contigs. The true order of the pieces
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Consensus quality: 157456 bases at least Q40 Consensus quality: 158960 bases at least Q30 Consensus quality: 159457 bases at least Q20 Insert size: 159639; sum-of-contigs quality coverage: 8.61x in Q20 bases; sum-of-contigs
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132659 137219; contig of Acci
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Search completed: November 28, 2001, 23:48:11 Job time: 8134 sec
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179783
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                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 246)
Walke, D.W. and Turner, C.A.
Walke, D.W. and Turner, C.A.
Human membrane proteins and polynucleotides encoding the same having homology to cd20 proteins and ige receptors
Patent: WO 0146417-A 3 28-JUN-2001;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
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AX179783.1 GI:15132145
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Human CD20 antigen	AAV81209	20	1476	9.0	40.4	5
	AAV63451	19	1476	9.0	40.4	4
CD20	AAT14713	17	1476	9.0	40.4	Ξ
_	7	13	1476	9.0	40.4	2
CD20 cDNA. AAN90	AAN90613	10	1476	9.0	40.4	Ξ
	AAS03178	22	1474	. 9.0	40.4	ö
cell su	AAA50584	21	1474	9.0	40.4	9
a	AAT14710	17	1474	9.0	40.4	8
CD20.4 cDNA. AAN	AAN90610	10	1473	9.0	40.4	37
Extended human sec	AAX97730	20	1060	9.0	40.6	8
Clone CD20.4 encod	AAQ21170	13	1474	9.3	42	5
Plasmodium falcipa	AAA70114	21	6888	9.6	43	4
Oligonucleotide Di	AAF58238	22	244	9.7	43.6	ü
Human FceRI beta g	AAQ51021	14	2545	9.9	44.4	2
Encodes beta subun	AAQ14734	12	2545	9.9	44.4	<u>~</u>
Encodes beta subun	AAQ04645	11	2545	9.9	44.4	ö
onucleotide	AAF58238	22	244	9.9	44.4	
	AAV03875	19	1661		46	8
protein co	AAT45120	17	1661		46	27
Human secreted exp	AAA45410	21	220			8
ne	AAF77694	22	708			
high aff	AAZ32842	21	1670			24
ıffinity i	AAX15104	20	1669	14.8	66.8	
~	AAA16693	21	1330	4		
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	AAF58262	22	936		71.4	
	AAF58259	22	936	ŗ	71.4	9
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  Human;
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                                                                     accttttcttttggagttatcttccttttcaccttgttaaaaccatatccaaggtttccc
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                                                        accttttcttttggagttatcttccttttcaccttgttaaaaccatatccaaggtttccc
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DB; AAU01210.
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                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                Query Match 77.2%;
Best Local Similarity 97.0%;
Matches 354; Conservative
                                                                                                                                                                                                                                                                                                 The present sequence encoding for a novel human membrane protein includes the flanking 5'- and 3'- sequences. Four amino acid sequences for novel human membrane proteins (AAU01210-AAU01213) are given in the present invention. These membrane proteins share structural similarity with membrane receptors such as the IgE receptor and mammalian CD20. The novel human membrane proteins are useful for identifying agonist, antagonist and modulators of the membrane proteins, and for producing
                                                                                                                                                                                                              be used for diagnosis, drug screening, pharmacogenomic applications, clinical trial monitoring and the treatment of physiological disorders and diseases. The polynucleotides encoding the membrane proteins can be used to generate PCR primers or probes to identify mutations associatewith a particular disease.
                                                                                                                                                                                                                                                                                     antibodies specific to the membrane proteins. The membrane proteins can
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 31-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide encoding novel human membrane identifying agonist, antagonist or modifiers antibodies useful in therapeutic, diagnostic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  physiological disorder;
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; Pred. No. 2.9e
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and pharmacogenomic
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diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; s
GENSET;
                                                                                                                                           The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of
                                                                                                                                                                                                 Claim 7;
                                                                                                                                                                                                                       Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety odiseases, and for diagnosis of those diseases.
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        Walke DW,
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logical disorder; ss.
        Turner CA;
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                          GENETICS INC
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                                                                                                                      "Human membrane protein
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Pred. No. 3e-8
0; Mismatches
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The present sequence encodes for novel human membrane protein #3. Human membrane protein #3 is 1 of 4 human membrane proteins (AAU01210-AAU01213) given in the present invention: These membrane proteins share structural similarity with membrane receptors such as the IgE receptor and mammalian CD20. The novel human membrane proteins are useful for identifying agonists, antagonists and modulators of the membrane proteins, and for producing antibodies specific to the membrane proteins. The membrane proteins can be used for diagnosis, drug screening, pharmacogenomic applications, clinical trial monitoring and the treatment of physiological disorders and diseases. The polynucleotides encoding the membrane proteins can be used to generate PCR primers or probes to identify mutations associated with a particular
                                                                          Sequence 417
                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide encoding novel human membrane protein, useful for identifying agonist, antagonist or modifiers or for producing antibodies useful in therapeutic, diagnostic and pharmacogenomic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-408646/43.
P-PSDB; AAU01212.
   Similarity
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                                                                          BP;
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75.7%;
94.1%;
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                                                                          91 C;
   Score 340.8;
Pred. No. 1.
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                             ttcctaattgcagtgaaaagaaaaccacagaaactctgatcaaaactacatttgtggtt
                                                                                 aaattatttgctagaaaaatgaaaatcttagggactatccagatcctgtttggaattatt
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RESULT AAC03080

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AAC03080; 06-OCT-2000

AAC03080 standard; cDNA;

372

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361 attctcaccaaaatag

376

Human secreted

EST,

SEQ ID

3078

(first

entry

gene therapy; chromosome

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EST;

expressed protein 5'

sequence mapping;

tag; secreted . NO

protein;

cDNA isolation;

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RESULT
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Best Local Sin
Matches 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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P-PSDB; AAG03074.
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11-SEP-2001
                                 AAH64745;
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                                                                standard; cDNA; 468
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96.3%;
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Pred. No. 1.3e-65;
                                                                ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to full length GENSET human nucleic acids encoding C potentially secreted proteins. The nucleic acids and the polypeptides c they encode may be used in the prevention, treatment and diagnosis of CC diseases associated with inappropriate GENSET gene expression. For CC example, they be used to treat disorders associated with decreased CC GENSET gene expression by rectifying mutations or deletions in a CC patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, CC antisense nucleic acid molecules may be administered to down regulate CC expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be compared to their expression. The sense and antisense nucleic acids may also be compared to their expression. The sense and antisense nucleic acids may also be compared to their expression and the sequences in samples, and hence to compare the compared to the compare
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06-MAR-2000;
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DB; AAG89142.
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2000US-0187470
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77.1%;
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Pred. No. 4.1e-53;
0; Mismatches 0;
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P-PSDB; AAU01211.
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                                                                                                                                                                                                              (LEXI-) LEXICON GENETICS INC
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                                                                                                                                                                                                                                                                                                                                                               human membrane protein #2 cDNA sequence.
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                                                                                                                                                                                                                                                                                                                                                 protein;
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1..246
/*tag= a
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Human membrane protein #2 is 1 of 4 human membrane proteins (ANU01210-ANU01213) given in the present invention. These membrane proteins share structural similarity with membrane receptors such as the IgE receptor and mammalian CD20. The novel human membrane proteins are useful for identifying agonists, antagonists and modulators of the membrane proteins, and for producing antibodies specific to the membrane proteins. The membrane proteins can be used for diagnosis, drug screening, pharmacogenomic applications, clinical trial monitoring and the treatment of physiological disorders and diseases. The polynucleotides encoding the membrane proteins can be used to generate PCR primers or probes to identify mutations associated with a particular Polynucleotide encoding novel human membrane protein, useful for identifying agonist, antagonist or modifiers or for producing antibodies useful in therapeutic, diagnostic and pharmacogenomic The present sequence encodes for novel human membrane protein Disclosure; Page 30; 32pp; English used to generate d with a particular

246 B₽; 60 A; 45 ü 47 <u>;</u> 94 ₽, 0 other;

AAZ36228-49 encode bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines,

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Claim

11;

Page 92-94; 120pp;

English

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RESULT
AAZ36238
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24-SEP-1998;
30-SEP-1998;
                                                                                                             WPI; 2000-038344/03.
P-PSDB; AAY53632.
                                                                                                                                                                                                                                                                                                                                                                                                                                Bone marrow secreted protein; bone marrow stromal cell; cytokine; cell proliferation; cell differentiation; hematopoiesis; anaemia; myeloid cell deficiency; lymphoid cell deficiency; myeloid cell; celly stimulating factor; granulocyte; monocyte; macrophage; myelo-suppression; megakaryocyte; platelet; platelet disorder; thrombocytopenia; hematopoeitic stem cell; stem cell disorder; aplastic anaemia; bone differentiation; paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon; ligament; nerve; wound healing; tissue repair; burn; incision; ulcer bone fracture; cartilage damage; artificial joint; ss.
                                                                            New isolated human production of other
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                                                                                                                                                                                                                                                                                                                                              sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding a bone marrow secreted protein designated BMS208.
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                                                                          human polynucleotide and secreted f other cytokines in certain cell /
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98US-0101603.
98US-0102540.
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1531..1536
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255..440
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Matches 160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to regulate hematopoiesis, and to treat myeloid or lymphoid cell deficiencies. In addition, they may be used to support the growth and proliferation of erythroid progenitor cells, and to treat various anaemias. They can have colony stimulating factor (CSF) activity and ca be used to support the growth and proliferation of myeloid cells such a granulocytes, monocytes or macrophages, to prevent or treat myelo-suppression, to support the growth and proliferation or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of hematopoeitic stem cells, either in place of or in and proliferation of hematopoeitic stem cells, either in place of or in
26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
                                                                                         01-FEB-2001
                                                                                                                                                                                                                                                      Oligonucleotide D1835
                                                      26-JUL-2000; 2000WO-US20476
                                                                                                                             WO200107665-A2
                                                                                                                                                              Synthetic
                                                                                                                                                                                                  gene expression; ss
                                                                                                                                                                                                                 Electron-transfer group;
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Best Local S
Matches 7
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         W0200107665-A2
                            Synthetic.
                                                Electron-transfer group; gene expression; ss.
                                                                               Oligonucleotide D1875
                                                                                                                                           AAF58254 standard;
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                                                                                                   24-APR-2001
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1.7%; P
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                                                          ETM; mismatch; genotyping;
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61; Mismatches
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Best Local
Electron-transfer group;
                      Oligonucleotide D1954.
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                                                                                        AAF58257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids hybridization
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17-MAR-2000;
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                                                                                      standard; DNA;
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ETM; mismatch; genotyping;
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monitoring gene expression.
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17-MAR-2000;
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Pred. No. 2.0
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AAF58259;

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                                                                                 Synthetic
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26-JUL-2000; 2000WO-US20476
                                                       WO200107665-A2
                                                                                                                         Electron-transfer group; ETM; mismatch; genotyping;
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26-JUL-1999; 99US-0145695 17-MAR-2000; 2000US-0190259

(CLIN-) CLINICAL MICRO SENSORS

WPI; 2001-159728/16

Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on single surface

Example 6; Page 128; 159pp; English.

The present invention relates to a composition comprising two nuclei acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.

Sequence 936 BP; 6 A; 138 C; 8 G; œ Ŧ. 776 other;

Query Match Best Local Similarity

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861; Mismatches 15
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17-MAR-2000; 2000US-0190259
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1.7%;
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                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses or a single surface
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gene expression; ss.
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ALIGNMENTS

; LIBRARY: BRAINOT04 ; CLONE: 927955 US-08-916-902A-2 Patent No. GENERAL INFORMATION: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1669 base pair TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166 APPLICANT: Bandman, Olga APPLICANT: Lal, Preeti APPLICANT: Corley, Neil C. APPLICANT: CORLEY, Neil C. TITLE OF INVENTION: HIGH AFFINITY TITLE OF INVENTION: RECEPTOR-LIKE NUMBER OF SEQUENCES: 4 TOPOLOGY: line CORRESPONDENCE ADDRESS: STATE: (STREET: 3174 POI CITY: Palo Alto STRANDEDNESS: ADDRESSEE: 2, Application 5. 5871930 94304 nucleic acid CA E: Incyte Pharmaceuticals, Inc 3174 Porter Drive USA linear single US/08916902A PROTEIN IMMUNOGLOBULIN

Query Match Best Local Similarity

14.8%; 53.4%;

Length 1669;

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Patent No. 5977072
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Best Local Similarity
Matches 140; Conserv
                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36.749
REFERENCE/DOCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,389
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APPLICANT: COriey, Neil C.
TITLE OF INVENTION: HIGH A
TITLE OF INVENTION: RECEPT
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                               IMMEDIATE SOURCE:
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                                                                 TOPOLOGY:
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                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94304
                                                                                              nucleic acid
                                                                                                              1669 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bandman, Olga
                             BRAINOT 04
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                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette
                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIGH AFFINITY IMMUNOGLOBULIN RECEPTOR-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.8%;
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                                                                                                                                                                                                                                      PF-0371 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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RESULT 3
US-08-318-492-3
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; LOCATION:
US-08-318-492-3
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Patent No. 5552312
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 140;
                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: BIH9

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-6240
                                                                                                                                                                                            TELEFAX: (617) 861-95.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                    FEATURE:
NAME/KEY:
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1661 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lim, Bing
APPLICANT: Adra, Chaker N:
APPLICANT: Lellas, Jean-Michel
TITLE OF INVENTION: RECOMBINAN
TITLE OF INVENTION: ASSAYS
                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445
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                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                            TOPOLOGY:
                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTATTTCCGTGTATATCGGGTACACAATTTGGGGGTCAGTAATGTTATTATTTCAGGAT 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGCCTTAGCATGGGAATAACAATGATGTGTATGGCATCTAATACTTATGGAAGTAACC 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lexington
                                                                                                                              nucleic acid
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                                                                                        linear
                                                                        DNA (genomic)
                                                                                                                                                                                                               861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECOMBINANT HTM4 GENE, PROTEIN AND ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                     US/08/318,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brook,
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                                                                                                                                                                                                                                                                         BIH94-03
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Pred. No. 1.3e-09;
0; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith & Reynolds,
                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.25
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Length 1661;

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US-08-707-340-3
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CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/318,492

FILING DATE: 06-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/675,648

TITTING DATE: 03-JUL-1996

TITTING DATE: 03-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3 Patent No.
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Best Local Similarity
Matches 116; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lim, Binc APPLICANT: Adra, Cha APPLICANT: Lelias, Cha APPLICANT: Lelias, CITILE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: BI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                    FEATURE:
                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                       NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 03-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                NAME/KEY:
                                                                                      TOPOLOGY:
                                                                                                   STRANDEDNESS:
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                                                                                                                                       LENGTH:
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5. 5705615
                                                                                                                 nucleic acid
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                                                                                                                                     1661 base pairs
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Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
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                                                                                                                                                                                        (617)
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                CDS
97..738
                                                                                     linear
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                                                                  DNA (genomic)
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55.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/707,340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brook, Smith & Reynolds,
                                                                                                                                                                                                                                           BIH94-03A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No.
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Best Local Sir
Matches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08994578 Patent No. 5972688
                                                    TELEFAX: (781) 861-954 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                       PRIOR APPLICATION UNBER: US 08/318,492
FILING DATE: 06-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         FILING DATE: 03-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/707,340
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lim, Bing
APPLICANT: Adra, Chaker N.
APPLICANT: Lelias, Jean-Michel
TITLE OF INVENTION: HTm4 METHODS OF TREATMENT AND ASSAYS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS
                                                                                                                            REFERENCE/DOCKET NUMBER: BI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 AAAATTACAAGTTCTTGGGGCCATCCAGATCCTGAATGCAGCAATGATTCTGGCTTTGGG 293
            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Mil
CITY: Lexington
STATE: Massachu
                                                                                                                                                                      NAME: Brook, David E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 03-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: Decem
                                                                                                              TELEPHONE:
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STRANDEDNESS:
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16; Conservative
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                                                                                            (781)
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                                                                                                              (781) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                        TUMBER: US/08/994,578
December 19, 1997
                                                                                                                                                                                                                                                                                                                                             03-SEP-1996
                                                                                            861-9540
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                                                                                                                                                                    22,592
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Pred. No. 0.00074;
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US-07-869-933-22
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; LOCATION:
US-08-994-578-3
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Sequence 22, Applica....
Patent No. 5770396
Patent No. 5770396
GENERAL INFORMATION: ISOLATION, CHARACTERIZATION, AND USE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR TITLE OF INVENTION: IMMUNOGLOBULIN
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
SEQUENCE 2545 base pairs
TENGTH: 2545 base pairs
                                                                                                                                                                                                                                                                                                          FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY_AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 40,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                    FEATURE:
                                                                                      FEATURE:
                                                                                                      MOLECULE TYPE:
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 NAME/KEY:
LOCATION:
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LOCATION:
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                                                                                                                          TOPOLOGY:
                                                                                                                                  STRANDEDNESS:
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TELEX: 899149
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46..786
sig_peptide
46..54
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97..738
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Pred. No. 0.00074;
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SEQ ID NO 22
LENGTH: 2545
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (46)..(54)
FEATURE:
NAME/KEY: CDS
LOCATION: (46)..(786)
US-09-103-663-22
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US-07-869-933-22
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US-09-103-663-22
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Best Local Similarity 54.5%;
Matches 134; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/103,663D CURRENT FILING DATE: 1998-06-23 EARLIER APPLICATION NUMBER: 07/869,933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER FILING DATE: 1992-04-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                               101 caactcaaagccccttgcaaaaattatttgctagaaaatgaaaatcttagggactatcc 160
                                                                                                                  188
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216 gttaaaaccatatccaaggtttcccttta-tatttctttcaggatatccattctggggct 274
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                                                          agatectgtttggaattatgaeettttettttggagttatetteetttteaeett----- 215
                                                                                                              caccacagcagacatggcagtcatttttgaagaaagagttggagttcctgggcgtaaccc 247
                                       aagttctggtttggtttgatatgcctttgttttggaacagttgtctgctccacactccaga 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22, Application US/09103663D o. 6171803
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                                                                                                                                                                                        Score 44.4; DB 4;
Pred. No. 0.0024;
0; Mismatches: 106;
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Pred. No. 0.0024;
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                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14,
                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, APPLICANT: FALKNER, F. (TITLE OF INVENTION: RECONUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         428
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                                                                                                                        y Match
9.2%; Score 41.6; DB 1;
Local Similarity 4.2%; Pred. No. 0.02;
hes 17; Conservative 214; Mismatches 173;
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                             66 atatgagtccacagaactttcagccacgaccttttcaactcaaagccccttgcaaaaatt 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Alexandria
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                                                                                            6
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                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BENT,
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SCHEIFLINGER, F.
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(703)683-4109
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                                                                   Matches
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3004 TTCTTTTAGTTTTTTTTTTCTATCCATTTTAGCAATTACAGCCCAACGGTCCTCCCGCAT 2945
                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                             NAME: Hanson, No. 6232460man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 54:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892,702
FILING DATE: 15-July 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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TITLE OF INVENTION: Methods For Diagnosis And Treating Cancers,
TITLE OF INVENTION: And Methods For Identifying Pathogenic Markers-In A Sample
TITLE OF INVENTION: No. 6232460mal Cells
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                  186 ttcttttggagttatcttccttttcaccttgttaaaaccatatccaaggtttccctttat 245
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STATE: No.
10103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/104,324B
FILING DATE: 25-June-1998
CLASSIFICATION: 435
                                                                                                                                                                                        LENGTH: 3393 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
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666 Fifth Avenue
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                                                                   Conservative
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                                                                Score 34.8; DB 4;
Pred. No. 1.2;
0; Mismatches 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION NOMBER: 08/892,702
APPLICATION NUMBER: 15-July-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6239256man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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APPLICANT: T reci
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                                                 2944 TTTTCTTATAGCTCCAAACTTCAGTGTAGGTCCAGGGGTTGTTAGAGATGAAGGGGCCTT 2885
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306 aattgcagtgaaaagaaaaccacagaaactctgggaattttgattacattgatgacttt 365
                                                                              246 atttctttcaggatatccattctggggctctgttttgttcattaattctggagccttcct 305
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TITLE OF INVENTION:
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805 Third Avenue
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ilarity 49.5%;
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VENTION: Methods For Diagnosis And Treating
VENTION: Cancers, And Methods For Identifying Pathogenic Markers
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                                                                                                                                                                                  Score 34.8; D
Pred. No. 1.2;
0; Mismatches
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US-08-568-147B-1
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Best Local Similarity
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TELEX: 230 901 SANS U
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sekiguchi, Aryou...
APPLICANT: Takeda, Katsumichi
TITLE OF INVENTION: DNA FRAGMENT CODING FOR SQUAMOUS CELL
TITLE OF INVENTION: CARCINOMA-ASSOCIATED ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
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APPLICATION NUMBER: 800
FILING DATE: 02-DEC-199
                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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NAME: DIGISTIO, FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 84:
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APPLICATION NUMBER: US
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221 aaccatatccaaggittccctttatatttctttcaggatatccattctggggctctgttt 280
                                                                                                                 425 CATCTAAATATTCCTGTAAAAATAGATACGTTTTTTCTCCGAAGAGCTTGTTGGCGATCT 366
                                                                                                                                     101 caactcaaagccccttgcaaaaattatttgctagaaaaatgaaaatcttagggactatcc 160
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TOPOLOGY: li
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STATE: New York
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 2;
0; Mismatches
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                                                                 Matches
                                                                                 Query Match
Best Local :
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                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/I
FILING DATE: 03-JAN-1994
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: DK 0988/93
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: I
FILING DATE: 30-DEC-
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                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 25-MAR-1993 ATTORNEY/AGENT INFORMATION:
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421
                 284 tcattaattctggagccttcctaattgcagtgaaaagaaaaaccacagaaactctgggaa 343
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                                                                                                                                                                                                                                                                                                                               NAME: BENT, Stephen A. REGISTRATION NUMBER: 29 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/179,557 FILING DATE: 07-JAN-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3000 K Street, N.W. CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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TAATGAGTTTAACCGGCATCATCATTGGAATTAAAATTCCAAGTGCAGTAAGCATCGCAG 362
                                                                 l Similarity
67; Conserv
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SYSTEM: PC-DOS/MS-DOS
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US-08-800-929A-5/c
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; LOCATION: (3677)...(3951)
; OTHER INFORMATION: n can be any nucleotide
US-09-212-971-5
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US-09-212-971-5/c
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Sequence 5, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 6669
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Best Local (
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EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT TITLE OF INVENTION: DISEASE FILE REFERENCE: 07891/009002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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2826 ATGTTTCTGAA 2816
                                                                                                                                                                                                                                                                                                                           2946 TGGCTGTAAAATAAGACCTTTCAAAGATTTTAAATTTTTTGTCCCCCTCAAAGAACTAAC 2887
                                                                                                                                                                                                                                               2886 ATTGTAGAGTTATTCAACTTATCACCTCCTGAAAACATTTTTGAACTTTTTGTTTTTCTAA 2827
                                                                                                                                                                                                                                                                          188 cttttggagttatcttccttttcaccttgttaaaaccatatccaaggtttccctttatat 247
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FILING DATE: 1998-12-16
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70; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 3.
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APPLICANT:

MacKenzie, Alexander Liston, Peter Baird, Stephen

APPLICANT: APPLICANT:

Tsang,

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Best Local Similarity 53.4%;
Matches 70; Conservative
                                                                                                                              GENERAL INFORMATION:
                                                                                                                                              Sequence 5, Application US/09617053A Patent No. 6300492
                                                                                          APPLICANT: Korneluk, APPLICANT: MacKenzie
                                      APPLICANT:
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   TITLE OF INVENTION:
                       APPLICANT:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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LENGTH: 6669 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bicker-Brady, Kristina
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                  2886 ATTGTAGAGTTATTCAACTTATCACCTCCTGAAAACATTTTTGAACTTTTTGTTTTTTCTAA 2827
                                                                                                                                                                                                                                                                                                                                                                                                          2946 TGGCTGTAAAATAAGACCTTTCAAAGATTTTAAATTTTTTGTCCCCCTCAAAGAACTAAC 2887
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
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                                                                                                                                                                                                                                                                                    248 ttctttcagga 258
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TOPOLOGY: linear
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OPERATING SYSTEM:
SOFTWARE: FastSE
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                 Tsang, Benjamin K
Pratt, Christine
                                                     Baird, Stephen
                                                                     Liston, Peter
                                                                                          MacKenzie, Alexander
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DETECTION AND MODULATION OF TAPS
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Christine
Li DETECTION AND MODULATION OF
LI DAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIV
                                                                                                             Robert G
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Pred. No. 3.
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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FEATURE:
NAME/REY: variation
LOCATION: (3677)...(3951)
OTHER INFORMATION: n can l
US-09-617-053A-5
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                                                                                                                                                                                                                      Query Match 7.4
Best Local Similarity 53.4
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE TITLE OF INVENTION: DISEASE FILE REFERENCE: 07891/09903 CURRENT APPLICATION NUMBER: US/09/617,053A CURRENT FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1997-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                2946 TGGCTGTAAAATAAGACCTTTCAAAGATTTTAAATTTTTTTGTCCCCCCTCAAAGAACTAAC 2887
2826 ATGTTTCTGAA 2816
                                                                          2886 ATTGTAGAGTTATTCAACTTATCACCTCCTGAAAACATTTTTGAACTTTTTGTTTTTCTAA 2827
                                                                                                                                                                         128 ttgctagaaaaatgaaaatcttagggactatccagatcctgtttggaattatgacctttt 187
                       248 ttctttcagga
                                                                                                         188 cttttggågttatcttccttttcaccttgttaaaaccatatccaaggtttccctttatat 247
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                                                                                                                                                                                                                                         7.4%;
                                                                                                                                                                                                                                                                                                                                   be any nucleotide
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Search completed: November 29, 2001, 00:20:23 Job time: 9655 sec

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Database
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Maximum Match 100%
Listing first 45 s
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AA781801
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AA781801 ai58g01.s,
AA436088 zu03a08.r
AA1436089 gf43h06.x
AI102083 ot38b02.s
AA707529 at41a12.s
AA470059 zt04h05.r
BE107659 UI-R-BT1-BE107659 UI-R-BT1-BE38325 EST00022
AA435988 zu03a08.s
AA416972 zt04h05.s
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BG495708	CNS016HF	CNS0039L	CNS017OM	B10659	CNS0039G	AL514901	CNS01400	CNS000B8	AL531049	CNS06WVA	BF319786	AQ580877	CNS06X9S	CNS0182P	AI807884	BE861164	BG538851	BE638317	BG720623	BG719295	BF475316	AA418443	AL544561	BG484817	BG571626	BG664654	AA234138	BF591089	BG720182	B86842	BE638321	AA758635
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ALIGNMENTS

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SOURCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                         source
                                                Tel: 314 286 1810
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 608 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 401.
Location/Qualifiers
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1 (basss 1 to 410)

1 (basss 1 to 410)

Kucaba, T., Lacy, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie ,T., Waterston, R. and Wilson, R. WashU-Merck EST Project 1997

Unpublished (1997)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA411806 410 bp mRNA EST 12-AUG-1997 zt67a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727372 3. similar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20;
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AA411806.1 GI:2070377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/db_xref="GDB:5924284"
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REFERENCE
AUTHORS
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AA781801/c
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ORGANISM
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similar to
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370; Conserv
                                                                                                                                                                   sequence.
            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                   Tumor Gene Index Unpublished (1997)
                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae 1 (bases 1 to 389)
                                                                                                                                             EST
 cDNA Library Preparation:
                                                                                                                     Homo sapiens
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/clone="IMAGE:727372"
/clone_lib="Soares_testis_NHT"
/sex="male"
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                                                                                                                                                                                        389 bp mRNA EST 31-
Soares_testis_NHT Homo sapiens cDNA clone
SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN
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M. Bento Soares, Ph.D.,
                                                         Anatomy
                                                                                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 410;
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one 1375056 3
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                                                                                                                                                                                   ATTTTGGGGTGCCACTCAGAGGATTGTGATTGTGAACAATGTTGTTGA 42
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                                                                                               AA436088
-zu03a08.rl
5' similar
                                                           AA436088
AA436088.1
 Eukaryota; Metazoa;
Mammalia; Eutheria;
                      Homo sapiens
                                   human
                                               EST
                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer: -40m13 fwd. ET from Amersham h quality sequence stop: 311.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares_testis_NHT"
                                                                                             516 bp mRNA EST 09-NOV-1997
Soares_testis_NHT Homo sapiens cDNA clone IMAGE:73
to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20
                                                            GI:2141002
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 Chordata;
Primates;
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; Pred. No. 3.1e-68;
0; Mismatches 0;
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                          IMAGE:730742
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Best Local 9
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 412
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                                                                                                 ttatatttctttcaggatatccattctggggctctgttttgttcattaattctggagcc
                                                                                                                                             accttttcttttggagttatcttccttttcaccttgttaaaaccatatccaaggtttccc
                                                                                                                                                                                         TCAGAATATGAGTCCACAGAACTTTCAGCCACGACCTTTTCAACTCAAAGCCCCCTTGCAA
                                                                                                                                                                                                                                     tcagaatatgagtccacagaactttcagccacgaccttttcaactcaaagccccttgcaa 120
                                                                                                                                                                                                                                                                   ATGGATTCAAGCACCGCACACAGTCCGGTGTTTCTGGTATTTCCTCCAGAAATCACTGCT 111
                                                                                                                                                                                                                                                                               acttt 365
                                                              ttcctaattgcagtgaaaagaaaaaccacagaaactctgggaattttgattacattgatg
                                                                                                                                                                              AAATTATTTGCTAGAAAATGAAAATCTTAGGGACTATCCAGATCCTGTTTGGAATTATG
                                           TTTATATTTCTTTCAGGATATCCATTCTGGGGCTCTGTTTTGTTCATTAATTCTGGAGCC
                                                                                                                                ACCTTTTCTTTGGAGTTATCTTCCTTTTCACTTTGTTAAAACCATATCCAAGGTTTCCC
                                                                                                                                                                                                                                                                                                               354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 516)
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:5927437"
/db_xref="taxon:9606"
/clone="IMAGE:730742"
/clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                            77.2%;
97.0%;
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328
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                                                                                                                                                                                       Local Similarity
GTGAAAAGAAAACCACAGAAACTCTGATAATATTGAGCCGAATAATGAATTT
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AI149899
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agaaaaatgaaaatcttagggactatccagatcctgtttggaattatgaccttttctttt 192
gtgaaaagaaaaaccacagaaactctgggaattttgattacattgatgacttt 365
                                                       ggagttatcttcctttttcaccttgttaaaacccatatccaaggtttcccttttatattttctt 252
                                                                                                                                                                                                                      AGAAAAATGAAAATCTTAGGGACTATCCAGATCCTGTTTGGAATTATGACCTTTTTCTTTT 449
                                                                                                                                          GGAGTTATCTTCCTTTTCACTTTGTTAAAACCATATCCAAGGTTTCCCTTTATATTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 742 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 455.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1752827"
/clone_lib_"Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                        47.98;
95.38;
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                                                                                                                                                                                                                                                                                                                      Score 215.4; DB 1
Pred. No. 1.6e-38;
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                                                                                                                                                                                                                                                   1 atggattcaagcaccgcacacagtccggtgtttctggtatttcctccagaaatcactgct 60
                                                                                                                                                                 tcagaatatgagtccacagaactttcagccacgaccttttcaactcaaagccccttgcaa 120
                                                                                                                                aaattatttgctagaaaaatgaaaatcttagggactatccagatcctgtttggaattatg 180
tttatatttctttcaggatatccattctggggctctgttttgttcattaattctggagcc 300
                                 TCATTAATTCTGGAGCCTTCCTAATTGCAGTGAAAAGAAAAACCACAGAAAACTCTGATCA 211
                                                                accttttcttttggagttatcttccttttcaccttgttaaaaccatatccaaggtttccc 240
                                                                                                 AAATTATTTGCTAGAAAAATGAAAATCTTAGGGGATATCCATTCTGGGGCTCTGTTTTGT
                                                                                                                                                                                                                                   ATGGATTCAAGCACCGCACACAGTCCGGTGTTTCTGGTATTTCCTCCAGAAATCACTGCT 391
                                                                                                                                                                                                                                                                                                     318;
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Insert Length: 598 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 393.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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AI002083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D
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                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1619019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares_testis_NHT"
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                                                                                                                                                                                                                                                                                                                     47.78;
70.78;
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                                                                                                                                                                                                                                                                                                                     Score 214.8; DB : Pred. No. 2.2e-38
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249 tctttcaggatatccattctggggctctgttttgttcattaattctggagccttcctaat 308

Matches Query Match Best Local

199;

Similarity 98.5 99; Conservative

43.8%;

Score 197.2; DB 1 Pred. No. 2.1e-34; Mismatches

DB 10;

281; 0

Indels

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
AA707529
AA707529.1 GI:2717447
                                                                                                                                                                                                                                                                                                                                       Insert Length: 456 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 218.
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                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                           Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Sequencing by: Washington University Genome

Clone distribution: NCI-CGAP clone distribution

Clone distribution: NCI-CGAP clone distribution
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                94
       /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories
                                                                                                                                                                                                   /lab_host="DH10B"
                                                                                                                                                                                                                                   /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                       /clone="1292062"
                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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               159;
                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 656 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 393.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA470059 415 bp mRNA EST 09-NOV-1997 zt94h05.rl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:73 5. similar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
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WashU-NCI human EST Project
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1. (bases 1 to 415)
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314 286 1810
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                                                                                       /organism="Homo sapiens"
/db_xref="GDB:5926570"
/db_xref="taxon:9606"
/clone="IMAGE:730041"
/clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                        /lab_host="DH10B"
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                          35.1%;
98.8%;
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           Score 157.8; DB 10;
Pred. No. 1.3e-25;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized testis library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
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Bonaldo, M.F., Lenno
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus
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                                                                                                                                                                                            'dev_stage="adult"
/lab_host="hHi0B (Life Technologies)"
/lab_host="hHi0B (Life Technologies)"
/lab_host="hHi0B (Life Technologies)"
/lab_host="hHi0B (Life Technologies)"
/lab_host="hHi0B (Pharmacia) with a modified
/note="height to the library derived from a mixture of
UI-R-BT1 is a subtracted library derived from a mixture of
the following tissues: hhippocampus, thalamus, mid-brain,
medulla, corpus striatum, cerebral cortex and testis. For
a detailed description of the library from which this
clone was derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
                                                                                                                               described in (Bonaldo, 6:791-806, 1996)
                        TAG_TISSUE=testis
TAG_SEQ=ACGCAG"
                                                                                                   TAG_LIB=UI-R-BT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="UI-R-BT1-ame-d-04-0-UI"
/clone_lib="UI-R-BT1"
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125
                                                                                                                                                                       Lennon and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161
                                   25
                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                 ccggtgtttctggtatttcctccagaaatcactgcttcagaatatgagtccacagaactt 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgttcattaattctggagccttcctaattgcagtgaaaagaaaaccacagaaactctgg 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agalcctgtttggaattatgaccttttcttttggagttatcttccttttcaccttgttaa 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aaccatatccaaggtttccctttatatttctttcaggatatccattctggggctctgttt 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAAAATGAGCCAGGCGATGAATTT 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCCATACCCAAGGTTCCCTTTTATATTTCTCTCAGGATATCCTTTCTGGGGCTCTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTTCATTAACTCTGGGACCTTTCTGATTGCTCTGAAAAGAAAAACTACAGACACTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 28-AUG-2000 EST00022 mouse testis apoptosis subtraction cDNA library Mus musculus cDNA clone MTA22 5', mRNA sequence. BE638325
                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: T7 promoter Primer High quality sequence stop: 22 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Pharmacology
Hunan Medical University
88 Xiangya road, Changsha, Hunan 410078, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: lj12@public.cs.hn.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Jiang H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed sequence tags from mouse testis apoptosis subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l (bases 1 to 224)
Jiang, H., Li, L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE638325.1 GI:9932068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  086-0731-4805036
086-0731-4497661
                                                                  Conservative
                                                                                                                                                                   58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                               /strain="C57BL"
/db_xref="taxon:10090"
/clone="MTA22"
                                                                                                                                                                /note="Vector: pUCm-T"
40 c 61 g
                                                                                                                                                                                                              /cell_type="spermatogenesis cells"
/dev_stage="adult"
                                                                                                                                                                                                  /lab_host="JM109"
                                                                                                                                                                                                                                               tissue_type="testis"
                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                  library"
                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                'clone_lib="mouse testis apoptosis subtraction cDNA
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82.0%;
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76.4%;
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                                                               Score 126.2; DB 1
Pred. No. 1.8e-18;
D; Mismatches 48
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Pred. No. 6.3e-23;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                  65
                                                                                                 DB 10;
                                                                48;
                                                                Indels
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BASE COUNT
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AUTHORS
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VERSION
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AA435988/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 CCCTTGTTCCTGGTGTTCCCTCCAGAGGTCACCACTCAAGAATACCAAACAACAGAACTT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTTTCACCTTGGTAAACCCATA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cttttcaccttgttaaaaccata 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atcttagggactatccagatcctgtttggaattatgaccttttctttttggagttatcttc 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGCCACAGCCTATAATCCCCCAAAACCGAGTGCAGAAGATCATTATTAGAAAATTGGAG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcagccacgaccttttcaactcaaagccccttgcaaaaattatttgctagaaaaatgaaa 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCTTAGGGACCACCCAGATCCTGTTTGGAATCATGAACTTTTCATTTGGAGTCATTTTC 25
                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@mage.llnl.gow) for further information. Possible reversed clone: similarity on wrong strand Insert Length: 733 Std Error: 0.00 Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 280.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA435988 382 bp mRNA EST 09-NOV-1997 zu03a08.sl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730742 3' similar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20 ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillier,L., Allen,M., Bowles,L.,
Krizman,D., Kucaba,T., Lacy,M., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White,Y., Wylie,T., WaterstowashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
1 (bases 1 to 382)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA435988.1 GI:2140902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,
,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., The:
White,Y., Wylie,T., Waterston,R. and Wilson,R.
                       135
               (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Scares and M. Fatima Bonaldo. " 73 c 67 g 107 t
                                                                                                                                                              /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                    /lab_host="DH10B"
                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:730742"
                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:5927437"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theising, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jost,
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Query Match
Best Local Similarity
Matches 113; Conserv

Conservative

25.1%; Score 113; DB 10; 100.0%; Pred. No. 1.5e-15; Live 0; Mismatches 0;

Length 382; Indels

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AA416972/c
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KEYWORDS
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                                                                                                                        Query Match
Best Local
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                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                  398
                                                145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
tctcaattttggggtgccactcagaggattgtgattgtgaaccaatgttgttga
                                                            tgggaattttgattacattgatgactttcagcattattgaattattcatttctctgcctt 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tctcaattttggggtgccactcagaggattgtgattgtgaacaatgttgttga
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                                              TGGGAATTTTGATTACATTGATGACTTTCAGCATTATTGAATTATTCATTTCTCTGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGGAATTTTGATTACATTGATGACTTTCAGCATTATTGAATTATTCATTTCTCTGCCTT
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                                                                                                          113;
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zt94h05.sl Soares_testis_NHT Homo sapiens cDNA clone
3' similar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                White,Y., Wylie,T., Waterst WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra, J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Thei White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Insert Length: 656 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA416972.1
                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 656 St.
Seq primer: -41m13 fwd.
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                                                                                                                                                                                                  138
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314 286 1810
                                                                                                          Conservative
                                                                                                                                                                                           Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "

77 c 67 g 105 t
                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:730041"
/clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:5926570"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
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                                                                                                                      25.1%;
100.0%;
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                                                                                                        0;
                                                                                                      Score 113; DB 10;
Pred. No. 1.5e-15;
0; Mismatches 0;
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                                                                                                                                   Length
                                                                                                        Indels
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one IMAGE:730041
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ah67b04.s1 :
similar to :
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AA758635.1
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CIT-HSP-2379G7.TF CIT-HSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Map Building
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1 (bases 1 to 538)
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1. .538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="CIT-HSP"
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CIT-HSP-2379G7.TR
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99.1%;
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                                                                                                                                                       TTCTCAATTTTGGGGTGCCACTCAGAGGATTGTGATTGTGAACAATGTTGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clones are available from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2379G7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1:
394 bp mRNA EST 29-DEC-1998 Soares_testis_NHT Homo sapiens cDNA clone 1320655 3' SW:CD2O_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20 ;, mRNA
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                                                                                                                                                                                                                                                                                                                               Score 112.4;
Pred. No. 1.9e
0; Mismatches
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1.9e-15;
1;
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Best Local
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                                                                                                                                                                                                           EST 28-AUG-200 ESTUUU13 mouse testis apoptosis subtraction cDNA library Mus musculus cDNA clone MTA13 5', mRNA sequence.
Contact: Jiang H
Department of Pharmacology
                                 Unpublished (2000)
                                                             Jiang, H., Li, L. and Expressed sequence t
                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                               Mus musculus
                                                                                                                                                                                              BE638321.1 GI:9932064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 661 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                 nouse mouse
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National Cancer Institute, Cancer Genome Anat
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                                                                                               (bases 1 to 218)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1998)
Other_GSSs: RPCI11-26F10.TV
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Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pleteredejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or fi
                                                                                                                                                                                                                                                                                                                                                            Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
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                                                                                                                                            Email: mdadams@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B86842.1 GI:2927974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: :
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hunan Medical University
88 Xiangya road, Changsh
Tel: 086-0731-4805036
Fax: 086-0731-4497661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    il: 1j12@public.cs.hn.cn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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/celi_type="spermatogenesis cells"
/dev_stage="adult"
/lab_host="JM109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="mouse testis apoptosis subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="MTA13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rounsley,S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.4%;
79.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Changsha, Hunan 410078, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 83; DB 10;
Pred. No. 8.7e-09;
D; Mismatches 25
                                                                                                                                                                                                                                                    Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suh, E., Wible, C., de Jong, P. and
                                                                                                                                                                                                                                                    MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Field, C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bass, S., Linher, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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       or from
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